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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ Examiner # _____ Date: _____
 An Unit _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg Room Location _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number*

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STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher <u>P. Schreiber</u>	NA Sequence (#) <u>8</u>	STN _____	
Searcher Phone # <u>308-4292</u>	AA Sequence (#) _____	Dialog _____	
Searcher Location <u>CM1 6A05</u>	Structure (#) _____	Quickie Other _____	
Date Requested <u>7/30/03</u>	Bibliographic _____	Ref. _____	
Searcher Priority Review Time <u>23</u>	Litigation _____	Lexis Nexis _____	
Final Prep Time <u>19</u>	Full text _____	Sequence Systems <u>Compu-gene Ig GCG</u>	
	Patent Family _____	USNA Internet _____	
	Other _____	Other Vendors _____	

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US-09-371-	306	SYOPDADFVTCPNNSDSEVOGLDRLQLEDKREHCYLLTKIKADPKKKGATLPOHIIPAGCSL
US-09-371-	306	SYOPDADFVTCPNNSDSEVOGLDRLQLEDKREHCYLLTKIKADPKKKGATLPOHIIPAGCSL
US-09-371-	306	SYOPDADFVTCPNNSDSEVOGLDRLQLEDKREHCYLLTKIKADPKKKGATLPOHIIPAGCSL
US-09-371-	306	SYOPDADFVTCPNNSDSEVOGLDRLQLEDKREHCYLLTKIKADPKKKGATLPOHIIPAGCSL
US-09-371-	306	SYOPDADFVTCPNNSDSEVOGLDRLQLEDKREHCYLLTKIKADPKKKGATLPOHIIPAGCSL
US-09-371-	305	SYOPDADFVTCPNNSDSEVOGLDRLQLEDKREHCYLLTKIKADPKKKGATLPOHIIPAGCSL
consensus		SYOPDADFVTCPNNSDSEVOGLDRLQLEDKREHCYLLTKIKADPKKKGATLPOHIIPAGCSL
US-09-371-	367	OFIFWMCLEIRAIIPKKAFLRALVDYTSDAEKRRLQETCSKOGAADYSREVRDACA
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US-09-371-	367	OFIFWMCLEIRAIIPKKAFLRALVDYTSDAEKRRLQETCSKOGAADYSREVRDACA
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US-09-371-	367	OFIFWMCLEIRAIIPKKAFLRALVDYTSDAEKRRLQETCSKOGAADYSREVRDACA
US-09-371-	366	OFIFWMCLEIRAIIPKKAFLRALVDYTSDAEKRRLQETCSKOGAADYSREVRDACA
consensus		OFIFWMCLEIRAIIPKKAFLRALVDYTSDAEKRRLQETCSKOGAADYSREVRDACA
US-09-371-	428	LLAFPSGCPPLSLLEHLPRKIQOPRPRYSCASSLHPGKLFHVENIVEFLSTATTEVLRKGV
US-09-371-	428	LLAFPSGCPPLSLLEHLPRKIQOPRPRYSCASSLHPGKLFHVENIVEFLSTATTEVLRKGV
US-09-371-	428	LLAFPSGCPPLSLLEHLPRKIQOPRPRYSCASSLHPGKLFHVENIVEFLSTATTEVLRKGV
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US-09-371-	427	LLAFPSGCPPLSLLEHLPRKIQOPRPRYSCASSLHPGKLFHVENIVEFLSTATTEVLRKGV
consensus		LLAFPSGCPPLSLLEHLPRKIQOPRPRYSCASSLHPGKLFHVENIVEFLSTATTEVLRKGV
US-09-371-	489	CTGWLALLVASVLOPNHIAHSHEDSGKALAPKISISPTTNSFHLPPDPSIPIMVGGCTGII
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consensus CTGWTALLVASVLPNIHASHEDSGKALAPKISISPRRTNSFHLDPDPSIPIMVGPGTGI

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US-09-371- 549 APFIFGLQHR nsknrtqmellegcgc flaaglrilgilyseksdsismgslil

consensus APFIFGLQHKREKLGQHPDNGAMWLEFGCRHKRDYLFKRELHFLKHGILTLKVSFS

US-09-371- 611 RDAVGESEAPAKYVQDNIOQLHGQOVARILLOENGHIYVCGDAKNMAKDVHDALVQIISKE
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US-09-371- 602 RfpgsgemlllgtrfkqgsmkyttsfmasrwrEsssrttalfmcvemgrlwpmympplck
consensus RdaPVgeeeapakyvQdnIqLhgqvarilLlqEnghIyvcgDaKnmaKdvhdAlvqIIske

US-09-371- 672 VGEKLEAMKTLATLKEEKRYLQDIWS
US-09-371- 672 VGEKLEAMKTLATLKEEKRYLQDIWS
US-09-371- 672 VGEKLEAMKTLATLKEEKRYLQDIWS
US-09-371- 671 VGEKLEAMKTLATLKEEKRYLQDIWS
US-09-371- 663 akrlelnknkqkpwplkknatfrifgh
consensus vgvEkleamKtlatLkeekrylqdiws

Alignment score = 2610.00

Scoring matrix:

	1	21	22	23	24
1		697	697	692	517
21			696	691	516
22				691	516
23					522
24					

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OM nucleic - nucleic search, using sw model

Run on: July 29, 2003, 10:56:19 ; Search time 425.084 Seconds
(without alignments)
10177.082 Million cell updates/sec

Title: US-09-371-347A-1

Perfect score: 2097

Sequence: 1 atgagaggttctgtact.....ttcagatatgtgtcataa 2097

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCr_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCrUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2097	100.0	2097	12	US-09-371-347-1
2	2097	100.0	3259	12	US-09-371-347-24
3	2095.4	99.9	2097	12	US-09-371-347-41
4	2095.4	99.9	2097	12	US-09-371-347-43
5	2081	99.2	2094	12	US-09-371-347-45
6	2079	99.1	2093	12	US-09-371-347-47
7	174.4	8.3	2475	12	US-09-809-5678-38
8	88.6	4.2	1872	11	US-09-817-800A-1351
9	88.6	4.2	2401	11	US-09-917-800A-1397
10	83.8	4.0	101	11	US-09-783-590-1364
11	61	2.9	298	10	US-09-294-0938-4842
12	59.6	2.8	2470	10	US-09-823-849A-278
13	58.4	2.8	230	10	US-09-823-849A-278
14	57.2	2.7	13508	8	US-08-781-986A-120
15	56	2.7	2136	11	US-09-938-842A-803
16	54.8	2.6	2403	11	US-09-880-107-3039

17	53.6	2.6	1863	10	US-09-765-873A-13	Sequence 13, App1
18	52.2	2.5	411	10	US-09-925-299-440	Sequence 440, App
19	52.2	2.5	411	12	US-09-925-299-440	Sequence 440, App
20	50.6	2.4	2088	15	US-10-128-714-7234	Sequence 7234, App
21	50.2	2.4	1448	10	US-09-939-980-113	Sequence 113, App
22	49.2	2.3	1944	15	US-10-272-017A-4	Sequence 4, App1
23	49.2	2.3	3037	10	US-09-911-781-10	Sequence 10, App1
24	49.2	2.3	4145	10	US-09-911-781-13	Sequence 3, App1
25	49.2	2.3	4145	12	US-09-876-800-82	Sequence 82, App1
26	49.2	2.3	4145	15	US-10-138-838-82	Sequence 82, App1
27	49.2	2.3	4145	15	US-10-139-031-82	Sequence 82, App1
28	49.2	2.3	4145	15	US-10-138-905-82	Sequence 82, App1
29	49.2	2.3	4145	15	US-10-138-916-82	Sequence 82, App1
30	47.6	2.3	1791	11	US-09-778-319-1	Sequence 1, App1
31	47.6	2.3	4957	15	US-10-201-213-1	Sequence 1, App1
32	46.4	2.2	1845	15	US-10-128-714-1234	Sequence 1234, App
33	46.4	2.2	1845	15	US-10-128-714-2234	Sequence 2234, App
34	46.4	2.2	2145	15	US-10-128-714-6234	Sequence 6234, App
35	46.4	2.2	3845	15	US-10-128-714-234	Sequence 234, App
36	46.4	2.2	4145	15	US-10-128-714-5234	Sequence 5234, App
37	46	2.2	1944	15	US-10-272-017A-1	Sequence 1, App1
38	46	2.2	4206	10	US-09-911-781-2	Sequence 2, App1
39	46	2.2	4206	12	US-09-976-800-81	Sequence 81, App1
40	46	2.2	4206	15	US-10-138-838-81	Sequence 81, App1
41	46	2.2	4206	15	US-10-139-031-81	Sequence 81, App1
42	46	2.2	4206	15	US-10-138-905-81	Sequence 81, App1
43	46	2.2	4206	15	US-10-138-916-81	Sequence 81, App1
44	46	2.2	640681	11	US-09-790-988-1	Sequence 1, App1
45	42.4	2.0	413	12	US-09-918-995-32917	Sequence 32917, A

ALIGNMENTS

RESULT 1
US-09-371-347-1
Sequence 1, Application US/09371347
Publication No. US20030082676A1
GENERAL INFORMATION:
APPLICANT: Roy A. Gravel et al.
TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371.347
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/071.622
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/232.028
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2097
TYPE: DNA
ORGANISM: Homo sapiens
US-09-371-347-1

Query Match 100.0%; Score 2097; DB 12; Length 2097;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAGGAGGTTTCTGTACTATATGCTACACAGGACAGGACGAAAGGCAATCGCAGAA	60
DB	1	ATGAGGAGGTTTCTGTACTATATGCTACACAGGACAGGACGAAAGGCAATCGCAGAA	60
QY	61	GAATGTGTAGCAGCTGTGTACATGATTTTCTCAGATCTTCACTAATAGTAA	120
DB	61	GAATGTGTAGCAGCTGTGTACATGATTTTCTCAGATCTTCACTAATAGTAA	120
QY	121	TCCGATATGATGACCTAATAAAGCAAGCTCTCTTGTGTGTGTTTACACAG	180
DB	121	TCCGATATGATGACCTAATAAAGCAAGCTCTCTTGTGTGTGTTTACACAG	180

OY	181	GGACACGGAGACCCACCCGACACAGCCCGCAAGTTTGTTAAGGAATACAGACCAACAA	240
Db	181	GGACACGGAGACCCACCCGACACAGCCCGCAAGTTTGTTAAGGAATACAGACCAACAA	240
OY	241	CTGCCGATGATTTCTTTGCTCACCCTGGGATATGGGTACTAGGGCTCTCGTGATTCAGAA	300
Db	241	CTGCCGATGATTTCTTTGCTCACCCTGGGATATGGGTACTAGGGCTCTCGTGATTCAGAA	300
OY	301	TACACCTTACTTTTGCATATGGGGGAGATTAATTGATTAACGACTTCAAGACTTGGAGCC	360
Db	301	TACACCTTACTTTTGCATATGGGGGAGATTAATTGATTAACGACTTCAAGACTTGGAGCC	360
OY	361	CGGCATTTCTATGACACTGACATCAGATGACATGATGATGATTAAGACTTGGTTGAG	420
Db	361	CGGCATTTCTATGACACTGACATCAGATGACATGATGATGATTAAGACTTGGTTGAG	420
OY	421	CCGTGATATGCTGACATCTGGCCAGCCCTCGAAGAACTTTTATAGTCAAGCAGAGACAA	480
Db	421	CCGTGATATGCTGACATCTGGCCAGCCCTCGAAGAACTTTTATAGTCAAGCAGAGACAA	480
OY	481	GAGGAGATTAAGGGGGGACATCCCGGTGGCATCACCTGATCCTTGAGACAGACTTGTG	540
Db	481	GAGGAGATTAAGGGGGGACATCCCGGTGGCATCACCTGATCCTTGAGACAGACTTGTG	540
OY	541	AAGTCAGAGCTGTACACATTGAATCTTCAAGTCGACCTTCTGAGATTTGATGATTCAGGA	600
Db	541	AAGTCAGAGCTGTACACATTGAATCTTCAAGTCGACCTTCTGAGATTTGATGATTCAGGA	600
OY	601	AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTAACACCAACCATCCAAATGTTGTA	660
Db	601	AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTAACACCAACCATCCAAATGTTGTA	660
OY	661	ATTGAAGACTTTGAGTCTCTCACTTACCCGTTGCGATCCGCCACTCTCAAGACCTCTCTG	720
Db	661	ATTGAAGACTTTGAGTCTCTCACTTACCCGTTGCGATCCGCCACTCTCTCAAGACCTCTCTG	720
OY	721	AATATTTCTGGTTTACCCTCCAGATATTTACAGGTACATCTGCGAGAGATCTCTTGGCCAG	780
Db	721	AATATTTCTGGTTTACCCTCCAGATATTTACAGGTACATCTGCGAGAGATCTCTTGGCCAG	780
OY	781	GAGAAAGCCCAAGATCTGTGACTTCAGCAGATCCAGTTTTCAGATGCCCAATTTCAAG	840
Db	781	GAGAAAGCCCAAGATCTGTGACTTCAGCAGATCCAGTTTTCAGATGCCCAATTTCAAG	840
OY	841	GCAGTTCACCTTACTAGCATGATGCCATTAACCACTGCTGTGATGAATTTGGACATT	900
Db	841	GCAGTTCACCTTACTAGCATGATGCCATTAACCACTGCTGTGATGAATTTGGACATT	900
OY	901	TCAATATCAGACTTTTCTATCAGCTGSGAATGCGCTCAGCGATGCTGCCCTTAACAGT	960
Db	901	TCAATATCAGACTTTTCTATCAGCTGSGAATGCGCTCAGCGATGCTGCCCTTAACAGT	960
OY	961	GATTCGAGGTACAAAGCCTACTCCAAAGACTGACGTTGAAGATTAAGAGAGACACTGC	1020
Db	961	GATTCGAGGTACAAAGCCTACTCCAAAGACTGACGTTGAAGATTAAGAGAGACACTGC	1020
OY	1021	GTCTTTTGAATAAAGGCGAGACACAAGAAAGAGAGCTACCTTAACCCACATATA	1080
Db	1021	GTCTTTTGAATAAAGGCGAGACACAAGAAAGAGAGCTACCTTAACCCACATATA	1080
OY	1081	CTTCGCGGATTTCTCTCAGTTTCAATTTTACCTGGTGTCTTGAATTCGAGCAATTCCT	1140
Db	1081	CTTCGCGGATTTCTCTCAGTTTCAATTTTACCTGGTGTCTTGAATTCGAGCAATTCCT	1140
OY	1141	AAAAAGCAATTTTTCGAGCCCTTGTGACTATACCAAGTCAAGTGTGAAAGACGAGG	1200
Db	1141	AAAAAGCAATTTTTCGAGCCCTTGTGACTATACCAAGTCAAGTGTGAAAGACGAGG	1200
OY	1201	CTACAGAGCTGTGACATGAACAGAGGGGACGCCATTAATAGCCGCTTTGTACGAGATGCC	1260
Db	1201	CTACAGAGCTGTGACATGAACAGAGGGGACGCCATTAATAGCCGCTTTGTACGAGATGCC	1260

OY	1261	TTGTGGCTTCCTGTGGATCTCTCTCTGCTTTTCCCTTTCTTCAGAGCCACCACTAGTCT	1320
Db	1261	TGTGGCTTCCTGTGGATCTCTCTCTGCTTTTCCCTTTCTTCAGAGCCACCACTAGTCT	1320
OY	1321	CTGCTCGAACATCTTCTTAACTTCAACCCAGACCATATTGCTGCGAAGCTCAAGTTTA	1380
Db	1321	CTGCTCGAACATCTTCTTAACTTCAACCCAGACCATATTGCTGCGAAGCTCAAGTTTA	1380
OY	1381	TTTCACCCAGGAAAGCTTCCATTTTGTCTTCAACATTGTGGAAATTGTCTACTAGCCACA	1440
Db	1381	TTTCACCCAGGAAAGCTTCCATTTTGTCTTCAACATTGTGGAAATTGTCTACTAGCCACA	1440
OY	1441	ACAGAGGTTCTCGGAGGAGGAGTATGTACAGAGCTGGCGGCTTGTTGGTTGCTTCAAGTT	1500
Db	1441	ACAGAGGTTCTCGGAGGAGGAGTATGTACAGAGCTGGCGGCTTGTTGGTTGCTTCAAGTT	1500
OY	1501	CTTCAGGCCAAACATACATGTCATCTCCCATGTAAACAGCGGGAAAGCCCTGCTCTTAAGATA	1560
Db	1501	CTTCAGGCCAAACATACATGTCATCTCCCATGTAAACAGCGGGAAAGCCCTGCTCTTAAGATA	1560
OY	1561	TTCCATCTCTCTCGAACAACAATTTCTTTCACATTACAGATGACCCCTCAATCCCATC	1620
Db	1561	TTCCATCTCTCTCGAACAACAATTTCTTTCACATTACAGATGACCCCTCAATCCCATC	1620
OY	1621	ATAATGTGTGGTCCAGAGAACCGGATAGCCCGCTTATTTGGTTCCTAACAACATAGAGAG	1680
Db	1621	ATAATGTGTGGTCCAGAGAACCGGATAGCCCGCTTATTTGGTTCCTAACAACATAGAGAG	1680
OY	1681	AAACTCCAGAACAAACACCCAGATGAGAAATTTGGAGCCATGTGTTTGGTCTGC	1740
Db	1681	AAACTCCAGAACAAACACCCAGATGAGAAATTTGGAGCCATGTGTTTGGTCTGC	1740
OY	1741	AGGATTAAGATTAAGGAGTTATCTTTCAGAAAAGAGTCAGACATTTCTTAAGCATAGGG	1800
Db	1741	AGGATTAAGATTAAGGAGTTATCTTTCAGAAAAGAGTCAGACATTTCTTAAGCATAGGG	1800
OY	1801	ATCTTAACTCATTAAGAGTTTCCCTTCTCAAGAGATCTCTCTTGTGGGAGAGAGAACCC	1860
Db	1801	ATCTTAACTCATTAAGAGTTTCCCTTCTCAAGAGATCTCTCTTGTGGGAGAGAGAACCC	1860
OY	1861	CCAGCAAAAGTATGTACAGACACACATCCAGTTCATGCGCAGAGGAGAGAAATCTTC	1920
Db	1861	CCAGCAAAAGTATGTACAGACACACATCCAGTTCATGCGCAGAGGAGAGAAATCTTC	1920
OY	1921	CTTCAGAGGAAGGCGCATTTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1980
Db	1921	CTTCAGAGGAAGGCGCATTTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1980
OY	1981	CATGATGCCCTTGTGCAAAATTAATTAAGCAAGAGAGTTGAGATTGAAAACATGAAGCAATG	2040
Db	1981	CATGATGCCCTTGTGCAAAATTAATTAAGCAAGAGAGTTGAGATTGAAAACATGAAGCAATG	2040
OY	2041	AAAAACCTGGCCACTTTAAAAAGAAAGAAAGCGTACCTTCAAGATATTGTGCTATAA	2097
Db	2041	AAAAACCTGGCCACTTTAAAAAGAAAGAAAGCGTACCTTCAAGATATTGTGCTATAA	2097

RESULT 2
US-09-371-347-24
Sequence 24, Application US/09371347
Publication No. US20030082676A1
GENERAL INFORMATION:
APPLICANT: ROY A. Grave! et al.
TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
TITLE OF INVENTION: DEFECTS,CARDIOVASCULAR DISEASE, AND CANCER
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371,347
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/071,622
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/232,028
PRIOR FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 3259
TYPE: DNA
ORGANISM: Homo sapiens
us-09-371-347-24

Query Match 100.0% Score 2097: DB 12: Length 3259:
Best Local Similarity 100.0% Pred. No. 0:
Matches 2097: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

1 ATGAGAGGTTCTGTTACTATATGCTACACAGAGGAGGACGCAAGGCCATCGCAGAA 60
80 ATGAGAGGTTCTGTTACTATATGCTACACAGAGGAGGACGCAAGGCCATCGCAGAA 139
61 GAAATGTGTAGCAGAGCTGTGTACATGATTTTCTGCAGATCTTCACTGATTAAGTGA 120
140 GAAATGTGTAGCAGAGCTGTGTACATGATTTTCTGCAGATCTTCACTGATTAAGTGA 199
121 TCCGATAGTATGACCTAAAAACGAAACAGCTCTCTGTTGTTGTTGTTCTTACACAG 180
200 TCCGATAGTATGACCTAAAAACGAAACAGCTCTCTGTTGTTGTTGTTCTTACACAG 259
181 GGCACCGGAGACCCACCCGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
260 GGCACCGGAGACCCACCCGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 319
241 CTGCCGGTGAATTTCTTTGCTCACCCTGGGTATGGGTACTGGGTCTCGTGATTCAGAA 300
320 CTGCCGGTGAATTTCTTTGCTCACCCTGGGTATGGGTACTGGGTCTCGTGATTCAGAA 379
301 TACACCTACTTTTGCATGGGGGGAATTAATGATTAACGACTTCAAGACTTGGAGCC 360
380 TACACCTACTTTTGCATGGGGGGAATTAATGATTAACGACTTCAAGACTTGGAGCC 439
361 CGGCATTTCTATGACACTGACATGACAGATGACTGTGAGTTTGAACCTGTGGTTAG 420
440 CGGCATTTCTATGACACTGACATGACAGATGACTGTGAGTTTGAACCTGTGGTTAG 499
421 CCGTGATTTGCTGACCTGTGGCCAGCCCTCAGAAAAGCATTTTAAAGTCAAGCAGAGAA 480
500 CCGTGATTTGCTGACCTGTGGCCAGCCCTCAGAAAAGCATTTTAAAGTCAAGCAGAGAA 559
481 GAGGAGATTAAGTGGGCGACCTCCGGTGGCATCACCTGATCCTTGAGAGACAGCTTGTG 540
560 GAGGAGATTAAGTGGGCGACCTCCGGTGGCATCACCTGATCCTTGAGAGACAGCTTGTG 619
541 AAGTCAGAGCTGCTACACATTAAGTCAAGTCAAGTCTTGAGATTCGATGATTCAGGA 600
620 AAGTCAGAGCTGCTACACATTAAGTCAAGTCAAGTCTTGAGATTCGATGATTCAGGA 679
601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTGTA 660
680 AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTGTA 739
661 ATTGAAGCTTTGAGTCTCACTTAACCGTTGGAGACCCCACTCTCAAGCCCTCTGTG 720
740 ATTGAAGCTTTGAGTCTCACTTAACCGTTGGAGACCCCACTCTCTCAAGCCCTCTGTG 799
721 AATATCTCTGTTTACCCCGAATATTTACAGGATCATCTGACAGAGTCTCTTGGCCAG 780
800 AATATCTCTGTTTACCCCGAATATTTACAGGATCATCTGACAGAGTCTCTTGGCCAG 859
781 GAGGAAAGCAAGTATCTGTGACTTACAGAGATCCAGTTTTCAGAGTCCCAATTTCAAG 840
860 GAGGAAAGCAAGTATCTGTGACTTACAGAGATCCAGTTTTCAGAGTCCCAATTTCAAG 919
841 GCAGTTCAAGTACTACAGATGATGCAATAAAAACCACTGCTGCTGAATTTGACATTT 900
920 GCAGTTCAAGTACTACAGATGATGCAATAAAAACCACTGCTGCTGAATTTGACATTT 979
901 TCAATATACAGATTTCTCTATCAGCTTGAGATGCTTCAAGGCTGATCTGCCCTAACAGT 960

980 TCAATATACAGATTTCTCTATCAGCTTGAGATGCTTCAAGGCTGATCTGCCCTAACAGT 1039
961 GATTCGTAGGTACAAAGCTCTCTCAAAAGATCGAGCTTGAAGTAAAGAGACACTGC 1020
1040 GATTCGTAGGTACAAAGCTCTCTCAAAAGATCGAGCTTGAAGTAAAGAGACACTGC 1099
1021 GTCCCTTTGAATAAAGCAGACACAAGAAAGAGAGTACCTTACCCAGCATATA 1080
1100 GTCCCTTTGAATAAAGCAGACACAAGAAAGAGAGTACCTTACCCAGCATATA 1159
1081 CCTCGGGAGTGTCTCTCAGTTCAATTTTACCTGCTCTTGAATCCGAGAAATTCCT 1140
1160 CCTCGGGAGTGTCTCTCAGTTCAATTTTACCTGCTCTTGAATCCGAGAAATTCCT 1219
1141 AAAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGCAGTGCCTGAAAGCCGAGG 1200
1220 AAAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGCAGTGCCTGAAAGCCGAGG 1279
1201 CTACAGAGCTGTGACAGTAAACAGAGGAGCCGATTTATACCCGCTTGTACAGATGCC 1260
1280 CTACAGAGCTGTGACAGTAAACAGAGGAGCCGATTTATACCCGCTTGTACAGATGCC 1339
1261 TGTGCTGCTGTTTGGATCTCTCTCGCTTCTCTTCCCTTTCGACAGCCAGCTAGTCTC 1320
1340 TGTGCTGCTGTTTGGATCTCTCTCTCGCTTCTCTTCCCTTTCGACAGCCAGCTAGTCTC 1399
1321 CTGCTCGAACAATTTCTTAACTTCAACCCAGACATATTTGTGTGCAAGCTCAAGTTA 1380
1400 CTGCTCGAACAATTTCTTAACTTCAACCCAGACATATTTGTGTGCAAGCTCAAGTTA 1459
1381 TTTCAACCCAGGAAAGCTCATTTTGTCTTCAACATTTGGAATTTCTGTACTAGCCACA 1440
1460 TTTCAACCCAGGAAAGCTCATTTTGTCTTCAACATTTGGAATTTCTGTACTAGCCACA 1519
1441 ACAGAGTTCGTGCGAAGAGATATGACAGCTGCTGCTGCTTGTGTTGCTTCACTT 1500
1520 ACAGAGTTCGTGCGAAGAGATATGACAGCTGCTGCTGCTTGTGTTGCTTCACTT 1579
1501 CTTGACGCAAAACATTCATGCAATCCCATGACAGCCGGAAGCCCTGCTCTTAAGTGA 1560
1580 CTTGACGCAAAACATTCATGCAATCCCATGACAGCCGGAAGCCCTGCTCTTAAGTGA 1639
1561 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCATTC 1620
1640 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCATTC 1699
1621 ATATGTGTGGTCCAGAACCGGACATGACCCCGTTTATTTGGGTTCTTCAACATAGAGAG 1680
1700 ATATGTGTGGTCCAGAACCGGACATGACCCCGTTTATTTGGGTTCTTCAACATAGAGAG 1759
1681 AAACCTCCAAAGAACACCCAGAGTGAATTTTGAAGCAATGTGTTGTTTTGGCTGTC 1740
1760 AAACCTCCAAAGAACACCCAGAGTGAATTTTGAAGCAATGTGTTGTTTTGGCTGTC 1819
1741 AGGCATTAAGGATTAAGGATTTATCTATTCAGAAAAGGCTCAGACATTTCTTAAGCATGG 1800
1820 AGGCATTAAGGATTAAGGATTTATCTATTCAGAAAAGGCTCAGACATTTCTTAAGCATGG 1879
1801 ATCTTAACTCATTAAGGATTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAACCC 1860
1880 ATCTTAACTCATTAAGGATTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAACCC 1939
1861 CCAGCAAGATATGTACAGAACATCCAGCTTCAATGGCCAGAGAGTGGCAGAAATCTCTC 1920
1940 CCAGCAAGATATGTACAGAACATCCAGCTTCAATGGCCAGAGAGTGGCAGAAATCTCTC 1999
1921 CTCAGAGAGAGGAGCATTTATGTGTGAGAGATGCAAGAAATATGCGCAAGAGATTA 1980
2000 CTCAGAGAGAGGAGCATTTATGTGTGAGAGATGCAAGAAATATGCGCAAGAGATTA 2059
1981 CATGATGCCCTTGTGCAAAATAAAGCAAGAGTTGAAGTGAAGAACTAGAAACAAATG 2040

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Db      2060 CATGATGCCCTTGTGCAAAATTAATAGCAAGAGTTGAGTTGAAAACTAGAACGATG 2119
QY      2041 AAAACCTGGCCACTTTAAAGAGAAAAACCTACTCTCAGGATATTGTGATCA-2097
        2120 AAAACCTGGCCACTTTAAAGAGAAAAACCTACTCTCAGGATATTGTGATCA 2176

RESULT 3
US-09-371-347-41
; Sequence 41, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-41

Query Match      99.9%; Score 2095.4; DB 12; Length 2097;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGAGAGAGTTCTCTACTATATGCTACACAGCAGGAGGACGAAAGCCATCGCAGAA 60
        1  ATGAGAGAGTTCTCTACTATATGCTACACAGCAGGAGGACGAAAGCCATCGCAGAA 60
Db
QY      61  GAAATGTGTGAGCAAGCTGTGTGATCATGATTTTCTGAGATCTTCACTGATTAAGTGA 120
        61  GAAATGTGTGAGCAAGCTGTGTGATCATGATTTTCTGAGATCTTCACTGATTAAGTGA 120
Db
QY      121 TCCGTAAGTATGACTTAAACCAACCAAGCTCTCTTTGTTGTGTGTTCTTACACAG 180
        121 TCCGTAAGTATGACTTAAACCAACCAAGCTCTCTTTGTTGTGTGTTCTTACACAG 180
Db
QY      121 TCCGTAAGTATGACTTAAACCAACCAAGCTCTCTTTGTTGTGTGTTCTTACACAG 180
        121 TCCGTAAGTATGACTTAAACCAACCAAGCTCTCTTTGTTGTGTGTTCTTACACAG 180
Db
QY      181 GGCACCGGAGACCCACCGGACACAGCCGCAAGTTGTTAAGGAATACAGAACCAACA 240
        181 GGCACCGGAGACCCACCGGACACAGCCGCAAGTTGTTAAGGAATACAGAACCAACA 240
Db
QY      181 GGCACCGGAGACCCACCGGACACAGCCGCAAGTTGTTAAGGAATACAGAACCAACA 240
        181 GGCACCGGAGACCCACCGGACACAGCCGCAAGTTGTTAAGGAATACAGAACCAACA 240
Db
QY      241 CTGCCGGTGTATTTCTTTGCTACCTGGGATAGGATGAGTCTCGGTGATTCAGAA 300
        241 CTGCCGGTGTATTTCTTTGCTACCTGGGATAGGATGAGTCTCGGTGATTCAGAA 300
Db
QY      241 CTGCCGGTGTATTTCTTTGCTACCTGGGATAGGATGAGTCTCGGTGATTCAGAA 300
        241 CTGCCGGTGTATTTCTTTGCTACCTGGGATAGGATGAGTCTCGGTGATTCAGAA 300
Db
QY      301 TACACCTACTTTTGAATGGGGGGAAGTAATTGATTAAGACACTTCAAGACCTGGAGCC 360
        301 TACACCTACTTTTGAATGGGGGGAAGTAATTGATTAAGACACTTCAAGACCTGGAGCC 360
Db
QY      301 TACACCTACTTTTGAATGGGGGGAAGTAATTGATTAAGACACTTCAAGACCTGGAGCC 360
        301 TACACCTACTTTTGAATGGGGGGAAGTAATTGATTAAGACACTTCAAGACCTGGAGCC 360
Db
QY      361 CGGCATTTCTATGACACTGAGCATGACATGCTGTGAGTTTGAAGACTGTGTAG 420
        361 CGGCATTTCTATGACACTGAGCATGACATGCTGTGAGTTTGAAGACTGTGTAG 420
Db
QY      361 CGGCATTTCTATGACACTGAGCATGACATGCTGTGAGTTTGAAGACTGTGTAG 420
        361 CGGCATTTCTATGACACTGAGCATGACATGCTGTGAGTTTGAAGACTGTGTAG 420
Db
QY      421 CCGTGAGATTTGCTGACTCTGGCAGCCCTCAGAAAGCAATTTTAGTCAAGCAGAGACAA 480
        421 CCGTGAGATTTGCTGACTCTGGCAGCCCTCAGAAAGCAATTTTAGTCAAGCAGAGACAA 480
Db
QY      421 CCGTGAGATTTGCTGACTCTGGCAGCCCTCAGAAAGCAATTTTAGTCAAGCAGAGACAA 480
        421 CCGTGAGATTTGCTGACTCTGGCAGCCCTCAGAAAGCAATTTTAGTCAAGCAGAGACAA 480
Db
QY      481 GAGAGAGATTAAGTGGGCGACTCCCGGTGGCATACCTGATCCTTGAGAGACAGACCTTGTG 540
        481 GAGAGAGATTAAGTGGGCGACTCCCGGTGGCATACCTGATCCTTGAGAGACAGACCTTGTG 540
Db
QY      481 GAGAGAGATTAAGTGGGCGACTCCCGGTGGCATACCTGATCCTTGAGAGACAGACCTTGTG 540
        481 GAGAGAGATTAAGTGGGCGACTCCCGGTGGCATACCTGATCCTTGAGAGACAGACCTTGTG 540
Db
QY      541 AAGTCAGAGCTGCTACATGATTCGAAAGTGTGAGATTCGATTCGATTCAGGA 600
        541 AAGTCAGAGCTGCTACATGATTCGAAAGTGTGAGATTCGATTCGATTCAGGA 600
Db

Db      541 AAGTCAGAGCTGCTACATGATTCGAAAGTGTGAGATTCGATTCGATTCAGGA 600
QY      601 AGAAGAGATTTGAGGTTTGAAGCAAAATGAGGACAGACAGAACCATTCATTTGTGA 660
        601 AGAAGAGATTTGAGGTTTGAAGCAAAATGAGGACAGACAGAACCATTCATTTGTGA 660
Db
QY      601 AGAAGAGATTTGAGGTTTGAAGCAAAATGAGGACAGACAGAACCATTCATTTGTGA 660
        601 AGAAGAGATTTGAGGTTTGAAGCAAAATGAGGACAGACAGAACCATTCATTTGTGA 660
Db
QY      661 ATTGAAGACTTTGAGTCTCCTACCTTACCGTTCGGTACCCCACTCTCAAGCCCTCTGTG 720
        661 ATTGAAGACTTTGAGTCTCCTACCTTACCGTTCGGTACCCCACTCTCTCAAGCCCTCTGTG 720
Db
QY      661 ATTGAAGACTTTGAGTCTCCTACCTTACCGTTCGGTACCCCACTCTCTCAAGCCCTCTGTG 720
        661 ATTGAAGACTTTGAGTCTCCTACCTTACCGTTCGGTACCCCACTCTCTCAAGCCCTCTGTG 720
Db
QY      721 AATATTCCTGTTTACCCCAAGATATTTTACAGTATCTGACAGAGCTCTCTGTGGCAG 780
        721 AATATTCCTGTTTACCCCAAGATATTTTACAGTATCTGACAGAGCTCTCTGTGGCAG 780
Db
QY      721 AATATTCCTGTTTACCCCAAGATATTTTACAGTATCTGACAGAGCTCTCTGTGGCAG 780
        721 AATATTCCTGTTTACCCCAAGATATTTTACAGTATCTGACAGAGCTCTCTGTGGCAG 780
Db
QY      781 GAGGAAGCAAGTATCTGTGCTCAGAGATTCAGATTTTCAAGTCCCAATTTTCAAG 840
        781 GAGGAAGCAAGTATCTGTGCTCAGAGATTCAGATTTTCAAGTCCCAATTTTCAAG 840
Db
QY      781 GAGGAAGCAAGTATCTGTGCTCAGAGATTCAGATTTTCAAGTCCCAATTTTCAAG 840
        781 GAGGAAGCAAGTATCTGTGCTCAGAGATTCAGATTTTCAAGTCCCAATTTTCAAG 840
Db
QY      841 GCAGTTCAACTTACTACGAATGATGCTCAATAAAACCACTCTGCTGTGAATGGACATTT 900
        841 GCAGTTCAACTTACTACGAATGATGCTCAATAAAACCACTCTGCTGTGAATGGACATTT 900
Db
QY      841 GCAGTTCAACTTACTACGAATGATGCTCAATAAAACCACTCTGCTGTGAATGGACATTT 900
        841 GCAGTTCAACTTACTACGAATGATGCTCAATAAAACCACTCTGCTGTGAATGGACATTT 900
Db
QY      901 TCAATATACAGACTTTTCTATCAGCTGAGATGCTTCAAGGATCTGCTCAACAGT 960
        901 TCAATATACAGACTTTTCTATCAGCTGAGATGCTTCAAGGATCTGCTCAACAGT 960
Db
QY      901 TCAATATACAGACTTTTCTATCAGCTGAGATGCTTCAAGGATCTGCTCAACAGT 960
        901 TCAATATACAGACTTTTCTATCAGCTGAGATGCTTCAAGGATCTGCTCAACAGT 960
Db
QY      961 GATTCGAGTACAAAGCTCTCCTCAAGACTGCGACTTGAAGATTAAGAGACATCTGC 1020
        961 GATTCGAGTACAAAGCTCTCCTCAAGACTGCGACTTGAAGATTAAGAGACATCTGC 1020
Db
QY      961 GATTCGAGTACAAAGCTCTCCTCAAGACTGCGACTTGAAGATTAAGAGACATCTGC 1020
        961 GATTCGAGTACAAAGCTCTCCTCAAGACTGCGACTTGAAGATTAAGAGACATCTGC 1020
Db
QY      1021 GTCTTTTGAATAATTAAGGACACACAAGAAAGAGAGCTTACCTTCCAGCATATA 1080
        1021 GTCTTTTGAATAATTAAGGACACACAAGAAAGAGAGCTTACCTTCCAGCATATA 1080
Db
QY      1021 GTCTTTTGAATAATTAAGGACACACAAGAAAGAGAGCTTACCTTCCAGCATATA 1080
        1021 GTCTTTTGAATAATTAAGGACACACAAGAAAGAGAGCTTACCTTCCAGCATATA 1080
Db
QY      1081 CCTGGGAGATTTCTCTCAGTTTCTTACCTGCTGTTGAAATCCGACAAATTCCT 1140
        1081 CCTGGGAGATTTCTCTCAGTTTCTTACCTGCTGTTGAAATCCGACAAATTCCT 1140
Db
QY      1081 CCTGGGAGATTTCTCTCAGTTTCTTACCTGCTGTTGAAATCCGACAAATTCCT 1140
        1081 CCTGGGAGATTTCTCTCAGTTTCTTACCTGCTGTTGAAATCCGACAAATTCCT 1140
Db
QY      1141 AAAAAGGATTTTTCGAGCCCTGTGAGATATACAGTGTGAAAGAGGAGG 1200
        1141 AAAAAGGATTTTTCGAGCCCTGTGAGATATACAGTGTGAAAGAGGAGGAGG 1200
Db
QY      1141 AAAAAGGATTTTTCGAGCCCTGTGAGATATACAGTGTGAAAGAGGAGGAGG 1200
        1141 AAAAAGGATTTTTCGAGCCCTGTGAGATATACAGTGTGAAAGAGGAGGAGG 1200
Db
QY      1201 CTACAGAGCTGTGCAATTAACCAAGGGGAGCCGATTAATACCCGTTGTGACGAGATGCC 1260
        1201 CTACAGAGCTGTGCAATTAACCAAGGGGAGCCGATTAATACCCGTTGTGACGAGATGCC 1260
Db
QY      1201 CTACAGAGCTGTGCAATTAACCAAGGGGAGCCGATTAATACCCGTTGTGACGAGATGCC 1260
        1201 CTACAGAGCTGTGCAATTAACCAAGGGGAGCCGATTAATACCCGTTGTGACGAGATGCC 1260
Db
QY      1261 TGTGCTGCTGTTGAGATCTCTCTGCTTCCCTTCTTTCGACGCCACTCAGTCTC 1320
        1261 TGTGCTGCTGTTGAGATCTCTCTGCTTCCCTTCTTTCGACGCCACTCAGTCTC 1320
Db
QY      1261 TGTGCTGCTGTTGAGATCTCTCTGCTTCCCTTCTTTCGACGCCACTCAGTCTC 1320
        1261 TGTGCTGCTGTTGAGATCTCTCTGCTTCCCTTCTTTCGACGCCACTCAGTCTC 1320
Db
QY      1321 CTGCTCGAACAATCTTCTTAACCTCAACCCAGACATATTGCTGGAAGCTCAAGTTTA 1380
        1321 CTGCTCGAACAATCTTCTTAACCTCAACCCAGACATATTGCTGGAAGCTCAAGTTTA 1380
Db
QY      1321 CTGCTCGAACAATCTTCTTAACCTCAACCCAGACATATTGCTGGAAGCTCAAGTTTA 1380
        1321 CTGCTCGAACAATCTTCTTAACCTCAACCCAGACATATTGCTGGAAGCTCAAGTTTA 1380
Db
QY      1381 TTTCAACCAGGAAGATCTCATTTTGTCTCAACATTTGGAATTTCTGTCTACGCGACA 1440
        1381 TTTCAACCAGGAAGATCTCATTTTGTCTCAACATTTGGAATTTCTGTCTACGCGACA 1440
Db
QY      1381 TTTCAACCAGGAAGATCTCATTTTGTCTCAACATTTGGAATTTCTGTCTACGCGACA 1440
        1381 TTTCAACCAGGAAGATCTCATTTTGTCTCAACATTTGGAATTTCTGTCTACGCGACA 1440
Db
QY      1441 ACAAGAGTTCGCGGAAGGAGTATGACAGGCTGCGCTGCTGTTGTTGCTTCAAGTT 1500
        1441 ACAAGAGTTCGCGGAAGGAGTATGACAGGCTGCGCTGCTGTTGTTGCTTCAAGTT 1500
Db
QY      1441 ACAAGAGTTCGCGGAAGGAGTATGACAGGCTGCGCTGCTGTTGTTGCTTCAAGTT 1500
        1441 ACAAGAGTTCGCGGAAGGAGTATGACAGGCTGCGCTGCTGTTGTTGCTTCAAGTT 1500
Db
QY      1501 CTTGAGCCAAACATACATGATCTCCATGAGACAGCCGGAAGCCCTGCTCTTAACATA 1560
        1501 CTTGAGCCAAACATACATGATCTCCATGAGACAGCCGGAAGCCCTGCTCTTAACATA 1560
Db
QY      1501 CTTGAGCCAAACATACATGATCTCCATGAGACAGCCGGAAGCCCTGCTCTTAACATA 1560
        1501 CTTGAGCCAAACATACATGATCTCCATGAGACAGCCGGAAGCCCTGCTCTTAACATA 1560
Db
QY      1561 TCCATCTCTCTCTCAACAAATTTCTTCACTTACCAAGATGACCCCTCAATCCCATC 1620
        1561 TCCATCTCTCTCTCAACAAATTTCTTCACTTACCAAGATGACCCCTCAATCCCATC 1620
Db
QY      1561 TCCATCTCTCTCTCAACAAATTTCTTCACTTACCAAGATGACCCCTCAATCCCATC 1620
        1561 TCCATCTCTCTCTCAACAAATTTCTTCACTTACCAAGATGACCCCTCAATCCCATC 1620
Db
QY      1621 AATATGTTGGTCCAGAGACCGGATAGCCCGTTTATTGGGTTCTTCAACATAGAGAG 1680
        1621 AATATGTTGGTCCAGAGACCGGATAGCCCGTTTATTGGGTTCTTCAACATAGAGAG 1680
Db
QY      1621 AATATGTTGGTCCAGAGACCGGATAGCCCGTTTATTGGGTTCTTCAACATAGAGAG 1680
        1621 AATATGTTGGTCCAGAGACCGGATAGCCCGTTTATTGGGTTCTTCAACATAGAGAG 1680
Db
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QY	1681	AAACTCCAGAACAACACCAGATGGAATTTTGAGCAATGTGGTCTTTTGGCTGC	1740
Db	1681	AAATCTCCAGAACACACCAGATGGAATTTTGAGCAATGTGGTCTTTTGGCTGC	1740
QY	1741	AGGCATTAAGATTAAGGATTTATCTATTCAGAAAAAGGTCAGACATTTTCCTTAACATGGG	1800
Db	1741	AGGCATTAAGGATTAAGGATTTATCTATTCAGAAAAAGGTCAGACATTTTCCTTAACATGGG	1800
QY	1801	ATCTTAACTCATCTAAAGTTTCCCTTCTCAAGAGATGCTCCGTGTTGGGGAAGAGAACCC	1860
Db	1801	ATCTTAACTCATCTAAAGTTTCCCTTCTCAAGAGATGCTCCGTGTTGGGGAAGAGAACCC	1860
QY	1861	CCACCAAAAGTATGTACAAAGACACATCCAGCTTATGCGCCAGCAGGTGGGAGATCCTC	1920
Db	1861	CCACCAAAAGTATGTACAAAGACACATCCAGCTTATGCGCCAGCAGGTGGGAGATCCTC	1920
QY	1921	CTCCAGGAGAAAGGCCCATTTATGTGTGTGTGGATGCAAAAGATATTGGCCCAAGATGTA	1980
Db	1921	CTCCAGGAGAAAGGCCCATTTATGTGTGTGTGGATGCAAAAGATATTGGCCCAAGATGTA	1980
QY	1981	CATGATGCCCTTGTGCAAAATTAATAAGCAAAAGAGTTGGAGTTGAAAACTAGAAGCATG	2040
Db	1981	CATGATGCCCTTGTGCAAAATTAATAAGCAAAAGAGTTGGAGTTGAAAACTAGAAGCATG	2040
QY	2041	AAAACCTGGGCACATTTAAAAAGAAAGAAAACGCTACCTTCAGGATATTGGTCTAA	2097
Db	2041	AAAACCTGGGCACATTTAAAAAGAAAGAAAACGCTACCTTCAGGATATTGGTCTAA	2097

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RESULT 4
US-09-371-347-43
: Sequence 43, Application US/09371347
: Publication NO. US20030082676A1
: GENERAL INFORMATION:
: APPLICANT: Roy A. Gravel et al.
: TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
: TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF
: TITLE OF INVENTION: DEFECTS,CARDIOVASCULAR DISEASE, AND CANCER
: FILE REFERENCE: 50004/003003
: CURRENT APPLICATION NUMBER: US/09/371,347
: CURRENT FILING DATE: 1999-08-10
: PRIOR APPLICATION NUMBER: 60/071,622
: PRIOR FILING DATE: 1998-01-16
: PRIOR APPLICATION NUMBER: 09/232,028
: PRIOR FILING DATE: 1999-01-15
: NUMBER OF SEQ ID NOS: 51
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 43
:
: LENGTH: 2097
:
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-371-347-43

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Query	March	99.9%	Score	2095.4	DB	12	Length	2097
Best	Local	Similarity	100.0%	Pred. No.	0			
Matches	2096	Conservative	0	Mismatches	1	Indels	0	Gaps
QY	1	ATGAGGAGGTTCTGTTACTATATGACACACGACGAGGACGCGAAGGCCATCGCAGAA	60					
Db	1	ATGAGGAGGTTCTGTTACTATATGACACACGACGAGGACGCGAAGGCCATCGCAGAA	60					
QY	61	GAAATGTGTGAGCAAGCTGTGCTACATGAGATTTTCTGACAGATCTTCACTGTAATTAGTGA	120					
Db	61	GAAATGTGTGAGCAAGCTGTGCTACATGAGATTTTCTGACAGATCTTCACTAATTAGTGA	120					
QY	121	TCCGATAGTAGTAGCTATTAACCGGAAACACTCTCCTCTGTGTTGTGGGTTTCACACG	180					
Db	121	TCCGATAGTAGTAGCTATTAACCGGAAACACTCTCCTCTGTGTTGTGGGTTTCACACG	180					
QY	181	GGCACCGGAGACCCACCGGACACAGCCCGCAAGTTTGTTAAGGAATACAGAACCAACA	240					
Db	181	GGCACCGGAGACCCACCGGACACAGCCCGCAAGTTTGTTAAGGAATACAGAACCAACA	240					

[illegible]

Accession	Sequence	Length
1021	GTCCCTTTGAAATTAAGGCAGACACAAGAGAGAGCGTACCTTAACCCAGCATATA	1080
1081	CGTGGGATGTCTCTCAGCTCATATTTTAACTGGTGCTTTGAAATCCGACAATTCCT	1140
1081	CCTGGGGGATGATCTCTCCAGCTTCATTTTAACTGGTGCTTTGAAATCCGACAATTCCT	1140
1141	AAAAAGGATTTTTCGCGAGCCCTTGAGACATATACAGTAGCACTGCTGAAGAACGCGAGG	1200
1141	AAAAAGGATTTTTCGCGAGCCCTTGAGACATATACAGTAGCACTGCTGAAGAACGCGAGG	1200
1201	CTACAGGAGCTGTGAGATTAACAAGAGGCGACCCATTATACCCCTTTGTTCGAGATGCC	1260
1201	CTACAGGAGCTGTGAGATTAACAAGAGGCGACCCATTATACCCCTTTGTTCGAGATGCC	1260
1261	TGTGCTCTCTGTTGGATCTCCTCCCTGCTTTCCTTCGAGCCACCACTAGTCTC	1320
1261	TGTGCTCTCTGTTGGATCTCCTCCCTGCTTTCCTTCGAGCCACCACTAGTCTC	1320

QY	1321	CTGCTCGAACAATCTTCCCTAAATCTCAACCCGACGACATATTCGTGTGGAAGCTCAAGTTTA	1380
Db	1321	CTGCTCGAACAATCTTCCCTAAATCTCAACCCGACGACATATTCGTGTGGAAGCTCAAGTTTA	1380
QY	1381	TTTTCACCCGAGAAAGCTCCATTTTGTCTCAACATTGTGGAATTTGTCTACAGCCACA	1440
Db	1381	TTTTCACCCGAGAAAGCTCCATTTTGTCTCAACATTGTGGAATTTGTCTACAGCCACA	1440
QY	1441	ACACAGGTTCTGGCGAAGGAGATGTATACAGAGCTGGCTGGCTTGTGTGCTTTCAGTT	1500
Db	1441	ACACAGGTTCTGGCGAAGGAGATGTATACAGAGCTGGCTGGCTTGTGTGCTTTCAGTT	1500
QY	1501	CTTCAGCCCAAAACATACATATGATTCATCCCATGAAGACAGCGGAAAGCCCTGGCTCTAAAGATA	1560
Db	1501	CTTCAGCCCAAAACATACATATGATTCATCCCATGAAGACAGCGGAAAGCCCTGGCTCTAAAGATA	1560
QY	1561	TTCATATCTCTCTCGAACAACAATAATTTCTTCACCTATTACCAATATGACCCCTCAATCCCATC	1620
Db	1561	TTCATATCTCTCTCGAACAACAATAATTTCTTCACCTATTACCAATATGACCCCTCAATCCCATC	1620
QY	1621	ATAATGTGTGGTCCGAGAACCCGGCATAGCCCGCTTATTTAGGTGCTCTAACAACATAGAGAG	1680
Db	1621	ATAATGTGTGGTCCGAGAACCCGGCATAGCCCGCTTATTTAGGTGCTCTAACAACATAGAGAG	1680
QY	1681	AAATCTCCAAAGAACACACCCAGATGAAATTTTGGAGCATCTCTCTGTGGGAGAGAAAGCC	1740
Db	1681	AAATCTCCAAAGAACACACCCAGATGAAATTTTGGAGCATCTCTCTGTGGGAGAGAAAGCC	1740
QY	1741	AGGCATTAAGATTAAGGAGATTATCTATCTACAGAAAAGGTCACACATTTTCCTTAACATAGGG	1800
Db	1741	AGGCATTAAGATTAAGGAGATTATCTATCTACAGAAAAGGTCACACATTTTCCTTAACATAGGG	1800
QY	1801	ATCTTAACTCATCTAAAGGTTTCTCTCTCAAGAGATCTCTCTGTGGGAGAGAAAGCC	1860
Db	1801	ATCTTAACTCATCTAAAGGTTTCTCTCTCAAGAGATCTCTCTGTGGGAGAGAAAGCC	1860
QY	1861	CCACCAAAAGTATGTACAAAGACAAATATCCAGCTTATGGCCAGACGAGTGGCGAATCTCTC	1920
Db	1861	CCACCAAAAGTATGTACAAAGACAAATATCCAGCTTATGGCCAGACGAGTGGCGAATCTCTC	1920
QY	1921	CTCCAGAGAAAGGCGCATATTTATGTGTGTGAGATGCCAAAGAAATATGGCCAAAGATGTA	1980
Db	1921	CTCCAGAGAAAGGCGCATATTTATGTGTGTGAGATGCCAAAGAAATATGGCCAAAGATGTA	1980
QY	1981	CATCATGCCCCCTGTGTGCAATTAATTAAGCAAGAGGTTGCAATTAAGAACTAAGAACATG	2040
Db	1981	CATCATGCCCCCTGTGTGCAATTAATTAAGCAAGAGGTTGCAATTAAGAACTAAGAACATG	2040
QY	2041	AAAACCCCTGGCCATTAAAAAGAGAAAAAACGCTACCTTCAGATATTTGGTCAATA	2097
Db	2041	AAAACCCCTGGCCATTAAAAAGAGAAAAAACGCTACCTTCAGATATTTGGTCAATA	2097

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;      TYPE: DNA
;      ORGANISM: Homo sapiens
US-09-371-347-45

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Query Match	99.28;	Score 2081;	DB 12;	Length 2094;
Best Local Similarity	99.98;	Pred. No. 0;		
Matches 2094;	Conservative	0;	Mismatches 0;	Indels 3; Gaps 1

QY	1	ATGAGGAGGTTTCCTGTA	CTTATGATGATACAGACAGGAGACAGGCAAGGCAATGGCAGAA	60
Db	1	ATGAGGAGGTTTCCTGTA	CTTATGATGATACAGACAGGAGACAGGCAAGGCAATGGCAGAA	60
QY	61	GAAATGTGTGACGACGCTG	GTGATCAGATGTTTCTGCAGATCTTCACTGTATTAGTCAA	120
Db	61	GAAATGTGTGACGACGCTG	GTGATCAGATGTTTCTGCAGATCTTCACTGTATTAGTCAA	120
QY	121	TCCGATTAAGTATGACCTA	ATAAACGAAACACTCTCTGTATGTTGGGTTTCAACACG	180
Db	121	TCCGATTAAGTATGACCTA	ATAAACGAAACACTCTCTGTATGTTGGGTTTCAACACG	180
QY	181	GGACCCGAGAGACCCACG	ACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA	240
Db	181	GGACCCGAGAGACCCACG	ACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA	240
QY	241	CTGCCGGTGAATTTCTT	TGCTCACCCTGGGTATGGGTACTGCGGTCTCGGTGATTACAGA	300
Db	241	CTGCCGGTGAATTTCTT	TGCTCACCCTGGGTATGGGTACTGCGGTCTCGGTGATTACAGA	300
QY	301	TACACCTA	CTTTCGAATGGGGGGAAGATATTATTAATAACACATTCGAAGACTTGGAGCC	360
Db	301	TACACCTA	CTTTCGAATGGGGGGAAGATATTATTAATAACACATTCGAAGACTTGGAGCC	360
QY	361	CGGCATTTCTATGACACT	GCACATGCAGATGACTGTAGGTTTGAACCTTGTGGTTGAG	420
Db	361	CGGCATTTCTATGACACT	GCACATGCAGATGACTGTAGGTTTGAACCTTGTGGTTGAG	420
QY	421	CCGTGGAATGCTGCACT	CTGTGGCCAGCCCTCAGAAAGCATTTTATAGTCAAGCAGAGACAA	480
Db	421	CCGTGGAATGCTGCACT	CTGTGGCCAGCCCTCAGAAAGCATTTTATAGTCAAGCAGAGACAA	480
QY	481	GAGAGATAAATGGCGCA	CTCCGGTGGCATCACCTGCATCTTGGAGACAGACTTGTG	540
Db	481	GAGAGATAAATGGCGCA	CTCCGGTGGCATCACCTGCATCTTGGAGACAGACTTGTG	540
QY	541	AAGTCAGAGCTGTACAC	ATTGAATCTCAAGTCAGGCTTCTGAGATTCGATGATTACAGA	600
Db	541	AAGTCAGAGCTGTACAC	ATTGAATCTCAAGTCAGGCTTCTGAGATTCGATGATTACAGA	600
QY	601	AGAAAGGATTTGTAGG	TTTTTAAGCAAAATGCACTGAGTGAACACCAACCAATCCATGTTGTA	660
Db	601	AGAAAGGATTTGTAGG	TTTTTAAGCAAAATGCACTGAGTGAACACCAACCAATCCATGTTGTA	660
QY	661	ATTGAAGACTTTGAGT	CTCTACCTACCCGTTCCGGTACCCCACTCTCACAAGCCTCTCTG	720
Db	661	ATTGAAGACTTTGAGT	CTCTACCTACCCGTTCCGGTACCCCACTCTCTCACAAGCCTCTCTG	720
QY	721	AATATTCCTGGTTTACC	CCAGAAATATTTACAGGTACATCTGCAGAGATCTTGTGGCAG	780
Db	721	AATATTCCTGGTTTACC	CCAGAAATATTTACAGGTACATCTGCAGAGATCTTGTGGCAG	780
QY	781	GAGAAAGCCAGATGAT	CTGTGACTTCAGACAGATCCAGTTTTCAAAGTCCCAATTTCAAG	840
Db	781	GAGAAAGCCAGATGAT	CTGTGACTTCAGACAGATCCAGTTTTCAAAGTCCCAATTTCAAG	840
QY	841	GCACTTCA	ACTTACTAGGAATGATGCCATAAAACCACTGCTGCTGATGAATTTGCAATT	900
Db	841	GCACTTCA	ACTTACTAGGAATGATGCCATAAAACCACTGCTGCTGATGAATTTGCAATT	900
QY	901	TCAAAATACAGACTTTT	CTATCAGCTGGAGATGCTTTCAGACGATCTGCCCTAACAGT	960
Db	901	TCAAAATACAGACTTTT	CTATCAGCTGGAGATGCTTTCAGACGATCTGCCCTAACAGT	960
QY	961	GATTCGAGGTACAAAG	CTTACTCAAAAGACTGACGTTGAGATTAAGAAGAGCACTGC	1020

|||||
Db GATTCGAGGTACAAAGCTACTCCAAAGCTGACGTTGAAGATTAAGAGACACATGC 1020
OY 961
1021 GTCTTTTGAATAAAGCGACACAAAGAAAGAGAGTACTTACCCACATATA 1080
Db 1021 GTCTTTTGAATAAAGCGACACAAAGAAAGAGAGTACTTACCCACATATA 1080
OY 1081 CCTCGGAGATGTCTCTCAGTTCATTTTACCTGTGTCTTGAATCCGAGCAATTCCT 1140
Db 1081 CCTCGGAGATGTCTCTCAGTTCATTTTACCTGTGTCTTGAATCCGAGCAATTCCT 1140
OY 1141 AAAAGGCATTTTGGCGAGCCCTTGTGACTATACAGTGAAGTCTGAAAAGCGCAGG 1200
Db 1141 AAAAGGCATTTTGGCGAGCCCTTGTGACTATACAGTGAAGTCTGAAAAGCGCAGG 1200
OY 1201 CTACAGAGCTGTGACAGTAACCAAGGGGACCCGATTAATACCCCTTGTACAGATGCC 1260
Db 1201 CTACAGAGCTGTGACAGTAACCAAGGGGACCCGATTAATACCCCTTGTACAGATGCC 1260
OY 1261 TGTGCTGCTGTGTGATCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Db 1261 TGTGCTGCTGTGTGATCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
OY 1321 CTGCTCGAATCTTCTCTAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA 1380
Db 1321 CTGCTCGAATCTTCTCTAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA 1380
OY 1381 TTTTACCCAGAAAGCTCCATTTTGTCTCAACATGTGGAAATTTCTCTACGCCACA 1440
Db 1381 TTTTACCCAGAAAGCTCCATTTTGTCTCAACATGTGGAAATTTCTCTACGCCACA 1440
OY 1441 ACAGAGGTTCTGCGAAGGAGTATGTACAGGCTGCGGCTTGTGTGCTTCACTT 1500
Db 1441 ACAGAGGTTCTGCGAAGGAGTATGTACAGGCTGCGGCTTGTGTGCTTCACTT 1500
OY 1501 CTTCAGCCAAACATACATGATTCCTCATGAGACAGCGGAAAGCCCTGCTCTAAGATA 1560
Db 1501 CTTCAGCCAAACATACATGATTCCTCATGAGACAGCGGAAAGCCCTGCTCTAAGATA 1560
OY 1561 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGAGCCCTCATCCCATC 1620
Db 1561 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGAGCCCTCATCCCATC 1620
OY 1621 ATATGTGTGGTCCAGAAACCGGATAGCCCGTTTATTTGGTCTCTCAACATAGAGAG 1680
Db 1621 ATATGTGTGGTCCAGAAACCGGATAGCCCGTTTATTTGGTCTCTCAACATAGAGAG 1680
OY 1681 AAACCTCCAAGAACACACCCAGATGGAATTTTGGAGCAATGTGTTTGGCTGC 1740
Db 1681 AAACCTCCAAGAACACACCCAGATGGAATTTTGGAGCAATGTGTTTGGCTGC 1740
OY 1741 AGGATAGAGTATAGGATATCTATCTAGAAAGAGCTCAGACATTTCTTACATAGATGG 1800
Db 1741 AGGATAGAGTATAGGATATCTATCTAGAAAGAGCTCAGACATTTCTTACATAGATGG 1800
OY 1801 ATCTTAATCTCATTAAGGTTTCTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAACCC 1860
Db 1801 ATCTTAATCTCATTAAGGTTTCTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAACCC 1860
OY 1861 CCAGCAAAAGTATGTACAGACATCCAGCTTCATGCGACAGAGTGGCAGAAATCTCTC 1920
Db 1861 CCAGCAAAAGTATGTACAGACATCCAGCTTCATGCGACAGAGTGGCAGAAATCTCTC 1920
OY 1921 CTCGAGGAGAGCGGATATTTATGTGTGTGAGATGGAAGAAATATGCGCAAGATCTA 1980
Db 1921 CTCGAGGAGAGCGGATATTTATGTGTGTGAGATGGAAGAAATATGCGCAAGATCTA 1980
OY 1981 CATGATGCCCTTGTGCAATATATAAGCAAGAGTGTGAAGTGAAGAACTAGAAAGCAATG 2040
Db 1981 CATGATGCCCTTGTGCAATATATAAGCAAGAGTGTGAAGTGAAGAACTAGAAAGCAATG 2040
OY 2041 AAAACCTGCGCCTTTTAAAGAGAAAGCAAGCTACCTTCAGAGATATTTGGCTATA 2097
Db 2041 AAAACCTGCGCCTTTTAAAGAGAAAGCAAGCTACCTTCAGAGATATTTGGCTATA 2097

Db 2038 AAAACCTGCGCCTTTTAAAGAGAAAGCAAGCTACCTTCAGAGATATTTGGCTATA 2094
RESULT 6
US-09-371-347-47
; Sequence 47, Application US/09371347
; Publication No. US2003082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371, 347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 2093
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-47
Query Match 99.1%; Score 2079; DB 12; Length 2093;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
OY 1 ATGAGAGAGTTTCTGTACTATATGCTACACAGCAGGAGGACGCAAGGCCATCGCAGAA 60
Db 1 ATGAGAGAGTTTCTGTACTATATGCTACACAGCAGGAGGACGCAAGGCCATCGCAGAA 60
OY 61 GAAATGTGTGAGCAAGCTGTGTACATGATTTTCTGAGATCTTCACTGATTAATGTA 120
Db 61 GAAATGTGTGAGCAAGCTGTGTACATGATTTTCTGAGATCTTCACTGATTAATGTA 120
OY 121 TCCGATAGTATGACCTTAAACCAAGCAACACTCTCTTGTGTGTGTTTCTTACACAG 180
Db 121 TCCGATAGTATGACCTTAAACCAAGCAACACTCTCTTGTGTGTGTTTCTTACACAG 180
OY 181 GGCACCGGAGACCCACCGGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
Db 181 GGCACCGGAGACCCACCGGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
OY 241 CTGCGGTTGATTTTCTTGTCTACCTGCGGATAGGTTACTGAGTCTCGTGTATCAGAA 300
Db 241 CTGCGGTTGATTTTCTTGTCTACCTGCGGATAGGTTACTGAGTCTCGTGTATCAGAA 300
OY 301 TACACCTACTTTTGCATGAGGAGGAGATTAATGATTAACGACTTCAAGAGCTTGGAGCC 360
Db 301 TACACCTACTTTTGCATGAGGAGGAGATTAATGATTAACGACTTCAAGAGCTTGGAGCC 360
OY 361 CGGCATTTCTTATGACACTGAGCATGAGATGATGATGATGATGATGATGATGATGATG 420
Db 361 CGGCATTTCTTATGACACTGAGCATGAGATGATGATGATGATGATGATGATGATGATG 420
OY 421 CCGTGATTTGCTGACCTGCGCAGCCCTCAGAAAGCAATTTTATGATCAAGAGAGACAA 480
Db 421 CCGTGATTTGCTGACCTGCGCAGCCCTCAGAAAGCAATTTTATGATCAAGAGAGACAA 480
OY 481 GAGGAGATTAAGTGGGCGACCTCCGCTGGCATACCTGATCTTGTAGAGACAGACTTGTG 540
Db 481 GAGGAGATTAAGTGGGCGACCTCCGCTGGCATACCTGATCTTGTAGAGACAGACTTGTG 540
OY 541 AAGTCAGAGCTGCTACATTTGAATCTCAAGTCAAGTCTTCTGAGATTTGATGATTCAGGA 600
Db 541 AAGTCAGAGCTGCTACATTTGAATCTCAAGTCAAGTCTTCTGAGATTTGATGATTCAGGA 600
OY 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACAGACCAATTCATGTTGTA 660
Db 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACAGACCAATTCATGTTGTA 660

Db 601 AGAAGGATTCGTAGCTTTTGAAGCAAAATCGACGTGAACAGACCAATTCATGTTGTA 660
 QY 661 ATTGAAGACTTTGAGTCTCTACTTACCCCTTGCGTACCCCACTCTCACAGCCTCTCTG 720
 Db 661 ATTGAAGACTTTGAGTCTCTACTTACCCCTTGCGTACCCCACTCTCACAGCCTCTCTG 720
 QY 721 AATATTCCGTTTACCCCAATATTTACAGTACATCTGACAGAGTCTCTGGCCAG 780
 Db 721 AATATTCCGTTTACCCCAATATTTACAGTACATCTGACAGAGTCTCTGGCCAG 780
 QY 781 GAGGAAAGCCAAATCTGTGACTTCAGAGATCCAGTTTCAAGTGCATTTTCAAG 840
 Db 781 GAGGAAAGCCAAATCTGTGACTTCAGAGATCCAGTTTCAAGTGCATTTTCAAG 840
 QY 841 GAGGTTCAACTTACTACAGATATGCTATTAACCACTCTCTGTGTAGATTTGACAT 900
 Db 841 GAGGTTCAACTTACTACAGATATGCTATTAACCACTCTCTGTGTAGATTTGACAT 900
 QY 901 TCAATATACAGCTTTTCTATCAGCTGAGATGGCTTCAGGCTGATCTGCCCTTAACAT 960
 Db 901 TCAATATACAGCTTTTCTATCAGCTGAGATGGCTTCAGGCTGATCTGCCCTTAACAT 960
 QY 961 GATTCGTGAGTCAAAAGCCTTACTCCAAAGACTGCAGCTTGAGATATAAAGAGAGACTGC 1020
 Db 961 GATTCGTGAGTCAAAAGCCTTACTCCAAAGACTGCAGCTTGAGATATAAAGAGAGACTGC 1020
 QY 1021 GTCTCTTTGAAAATTAAGGACACACAAAGAAAGAGAGCTTACTTACCCAGCATATA 1080
 Db 1021 GTCTCTTTGAAAATTAAGGACACACAAAGAAAGAGAGCTTACTTACCCAGCATATA 1080
 QY 1081 CCTGGGAGTGTCTCTCAGTTCATTTTCTGTGCTGTAATCCGACCATTTCT 1140
 Db 1081 CCTGGGAGTGTCTCTCAGTTCATTTTCTGTGCTGTAATCCGACCATTTCT 1140
 QY 1141 AAAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTGCAGTGTGAAAAGGCGCAGG 1200
 Db 1141 AAAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTGCAGTGTGAAAAGGCGCAGG 1200
 QY 1201 CTACAGGAGCTGTGAGTAACCAAGGCGCAGCCGATTTAGCCGCTTTGTACAGATGCC 1260
 Db 1201 CTACAGGAGCTGTGAGTAACCAAGGCGCAGCCGATTTAGCCGCTTTGTACAGATGCC 1260
 QY 1261 TGTGCTCTCTGTGATCT 1320
 Db 1261 TGTGCTCTCTGTGATCT 1320
 QY 1321 CTGCTCGAATCTTCTTAACCTTCAACCCAGACCATATGCTGTGCAAGCTCAAGTTTA 1380
 Db 1321 CTGCTCGAATCTTCTTAACCTTCAACCCAGACCATATGCTGTGCAAGCTCAAGTTTA 1380
 QY 1381 TTTACCCAGGAAAGCTCATTTTGTCTTCAACATTTGTGGAATTTCTCTACTGCCCCA 1440
 Db 1381 TTTACCCAGGAAAGCTCATTTTGTCTTCAACATTTGTGGAATTTCTCTACTGCCCCA 1440
 QY 1441 ACAGAGGTTCTGCGAAGGAGTATGTACAGGCTGCGGCTTGTGTTGCTTCATTT 1500
 Db 1441 ACAGAGGTTCTGCGAAGGAGTATGTACAGGCTGCGGCTTGTGTTGCTTCATTT 1500
 QY 1501 CTTACAGCCAAACATACATGATCCCATGAAAGACAGCGGAAAGCCCTGCTCTAAGATA 1560
 Db 1501 CTTACAGCCAAACATACATGATCCCATGAAAGACAGCGGAAAGCCCTGCTCTAAGATA 1560
 QY 1561 TCCATCTCTCTGCAACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATTC 1620
 Db 1561 TCCATCTCTCTGCAACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATTC 1620
 QY 1621 AATAATGTTGGTCCAGAAACCGCATAGCCCGTTTATTTGGTCTCTCAACATAGAAAG 1680
 Db 1621 AATAATGTTGGTCCAGAAACCGCATAGCCCGTTTATTTGGTCTCTCAACATAGAAAG 1680
 QY 1681 AACTCCAGAAACACACCGATGGAATTTTGGAGCAATGTGTTGTTTGGTCTC 1740
 Db 1681 AACTCCAGAAACACACCGATGGAATTTTGGAGCAATGTGTTGTTTGGTCTC 1740
 QY 1741 AACTCCAGAAACACACCGATGGAATTTTGGAGCAATGTGTTGTTTGGTCTC 1800
 Db 1741 AACTCCAGAAACACACCGATGGAATTTTGGAGCAATGTGTTGTTTGGTCTC 1800

QY 1741 AGGCATTAAGATAGGATTTATCTATTCAGAAAAAGAGCTCAGACATTTCTTAACCATGG 1800
 Db 1737 AGGCATTAAGATAGGATTTATCTATTCAGAAAAAGAGCTCAGACATTTCTTAACCATGG 1796
 QY 1801 ATCTTACTCATCTAAAGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1860
 Db 1797 ATCTTACTCATCTAAAGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1856
 QY 1861 CCAGAAAGTATGTCAAGACACATCCAGCTTCATGGCCAGAGTGGCCGATTCCTC 1920
 Db 1857 CCAGAAAGTATGTCAAGACACATCCAGCTTCATGGCCAGAGTGGCCGATTCCTC 1916
 QY 1921 CTCAGAGAAAGGCGCATATTTATGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1980
 Db 1917 CTCAGAGAAAGGCGCATATTTATGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1976
 QY 1981 CATGATGCCCTTGTCCAAATTAAGCAAAAGGTTGAGTTGAAAACCTAGAACATG 2040
 Db 1977 CATGATGCCCTTGTCCAAATTAAGCAAAAGGTTGAGTTGAAAACCTAGAACATG 2036
 QY 2041 AAAACCTGGCCACTTTAAAGAGAAAGAGCTCCTTCAAGATATTTGTCATAA 2097
 Db 2037 AAAACCTGGCCACTTTAAAGAGAAAGAGCTCCTTCAAGATATTTGTCATAA 2093

RESULT 7
 US-09-567B-38
 ; Sequence 38, Application US/09909567B
 ; Publication No. US2003022257A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Macina, Roberto A.
 ; APPLICANT: Nair, Manoj
 ; APPLICANT: Chen, Seiyu
 ; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
 ; FILE REFERENCE: DEX-0214
 ; CURRENT APPLICATION NUMBER: US/09/909,567B
 ; PRIOR FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: 60/219,834
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 38
 ; LENGTH: 2475
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1001)..(1001)
 ; OTHER INFORMATION: a, c, g or t
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1011)..(1011)
 ; OTHER INFORMATION: a, c, g or t
 ; US-09-909-567B-38

Query Match 8.3%; Score 174.4; DB 12; Length 2475;
 Best Local Similarity 96.7%; Pred. No. 1.2e-44;
 Matches 178; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 510 ATCACTGTCATCTCTGAGAGACAGCTTTGTGAATCAGAGCTGTACACATTTGATCTCA 569
 Db 1 ATCACTGTCATCTCTGAGAGACAGCTTTGTGAATCAGAGCTGTACACATTTGATCTCA 60
 QY 570 AGTCGAGCTTGTGATTCGATGATTCAGGAAGAAGATTCGAGTTTGAAGCAAAA 629
 Db 61 AGTCGAGCTTGTGATTCGATGATTCAGGAAGAAGATTCGAGTTTGAAGCAAAA 120
 QY 630 TGCAGTAAACGACCAATTCATGTTGTATTAAGAGACTTTGAGTCTTACCTACCCG 689
 Db 121 TGCAGTAAACGACCAATTCATGTTGTATTAAGAGACTTTGAGTCTTACCGATCTC 180
 QY 690 TTGC 693

Db 181 TTGC 184

RESULT 8

US-09-917-800A-1351
; Sequence 1351, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1351
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 E01524
US-09-917-800A-1351

Query Match 4.2%; Score 88.6; DB 11; Length 1872;
Best Local Similarity 56.2%; Pred. No. 4.5e-17;
Matches 222; Conservative 0; Mismatches 149; Indels 24; Gaps 2;

QY 1588 TTCCACTTACGAGTGAACCCCTCAATCCCATTAATGTTGGGTCCAGAACCGGATATA 1647
Db 1387 TTCCGCTTGCTTTCAAGTCCACACACCTGTATCATGTGGGGCCCGGACGTGGGATT 1446
QY 1648 GCCCGCTTTATTTGGGTTCTCTACAACATAGAGAGAACTCCAAAGAACACACCCAGATGA 1707
Db 1447 GCCCTTTATTTGGGTTCTCTACAACATAGAGAGAACTCCAAAGAACACACCCAGATGA 1707
QY 1708 AATTTTGGAGCAATGTGTTGTTTGGCTGCAGCATTAAGATTAAGGATTATCTATTC 1767
Db 1505 ---TGGAGAGAGAGCTGTACTATGCTGCGGGCTGCGATGAGACTATCTGTAC 1560
QY 1768 AGAAAGAGCTCAACATTTCTTAAGCATGGGATCTTAATCTTAAGGTTTCCTC 1827
Db 1561 CGTAAAGAGCTAGCCCGCTTCCACAGAGAGCGTCCCTCACGACTTAATGTGCTTT 1620
QY 1828 TCAAGAGATGCTCTGTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1887
Db 1621 TCCCG-----GGATC 1662
QY 1888 CAGCTTATGCGCAGATC 1947

Db 1663 AAGAGAGACAGGAGAACCTGTGAGACTGATCCAGAGGCGGTGCCACATCTATGTG 1722
QY 1948 TGTGAGATGCAAAAGATATGCGCAAGATGTACA 1982
Db 1723 TCCGGGATGCTGCAATATATGCGCAAGATGTGCA 1757

RESULT 9

US-09-917-800A-1397
; Sequence 1397, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1397
; LENGTH: 2401
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 M10068
US-09-917-800A-1397

Query Match 4.2%; Score 88.6; DB 11; Length 2401;
Best Local Similarity 56.2%; Pred. No. 5.4e-17;
Matches 222; Conservative 0; Mismatches 149; Indels 24; Gaps 2;

QY 1588 TTCCACTTACGAGTGAACCCCTCAATCCCATTAATGTTGGGTCCAGAACCGGATATA 1647
Db 1556 TTCCGCTTGCTTTCAAGTCCACACACCTGTATCATGTGGGGCCCGGACGTGGGATT 1615
QY 1648 GCCCGCTTTATTTGGGTTCTCTACAACATAGAGAGAACTCCAAAGAACACACCCAGATGA 1707
Db 1616 GCCCTTTATTTGGGTTCTCTACAACATAGAGAGAACTCCAAAGAACACACCCAGATGA 1707
QY 1708 AATTTTGGAGCAATGTGTTTGGCTGCAGCATTAAGATTAAGGATTATCTATTC 1767
Db 1674 ---TGGAGAGAGAGCTGTACTATGCTGCGGGCTGCGATGAGACTATCTGTAC 1729
QY 1768 AGAAAGAGCTCAACATTTCTTAAGCATGGGATCTTAATCTTAAGGTTTCCTC 1827
Db 1730 CGTAAAGAGCTAGCCCGCTTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1789
QY 1828 TCAAGAGATGCTCTGTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 1887
Db 1790 TCCCG-----GGATC 1831

```

: LENGTH: 298
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: incyte ID NO. US20010051335A1 700355168H1
US-09-294-0938-4842

Query Match
Best Local Similarity 58.0%; Pred. No. 1e-08;
Matches 148; Conservative 0; Mismatches 100; Indels 7; Gaps 2;

QY 1587 TTTCACCTTACCAGATGACCCCTCAATCCCATCATTAATGTGGTCCAGAAACCGGAT 1648
Db 46 TTTCAGATTACCTCTGCTGACCCATCCACCATCATATCATGATGGTCTCGGACAGGC-T 104

QY 1647 AGCCCCGTTTNTGGTTCCTCAACAACATAGAGAGAAATCCCAAGAACACACCAGATGG 1706
Db 105 GGGCTCTTTTATAGAGATTTCTTGACGAAAGGTTAGCACTGAACAACT- - - - -CTGAGC 158

QY 1707 AAATTTTGAGCAATATGTTGTTTGTGCTGCAGCATATAGATATAGATATTAATCAATT 1766
Db 159 AGAAGTGGGACCTTCATACCTCTTTCTTTTGATGCGAGAAACGGTATATAGACTCATATTA 218

QY 1767 CAGAAAGAGCTCAGACATTTCTTAAAGATGGGATCTTAACTCATCTAAGTTTCCTT 1822
Db 219 TGAAGATGAGCTGCAAACTTCTTGAGGAGAGGGGGCTGCTGTAGCTAATATTTGCATT 278

QY 1827 CTCAGAGATGCTCC 1841
Db 279 CTCGCGGAGAGGCC 293

RESULT 12
US-09-822-849A-278
: Sequence 278, Application US/09822849A
: Patent No. US20020045170A1
: GENERAL INFORMATION:
: APPLICANT: Wong, Gordon G.
: APPLICANT: Clark, Hilary
: APPLICANT: Fechtel, Kim
: APPLICANT: Agostino, Michael J.
: APPLICANT: Howes, Steven H.
: APPLICANT: Resnick, Richard J.
: APPLICANT: Gulukota, Kamalakari
: APPLICANT: Graham, James R.
: APPLICANT: Genetics Institute, Inc.
: TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
: FILE REFERENCE: GIN 6403
: CURRENT APPLICATION NUMBER: US/09/822,849A
: PRIOR APPLICATION NUMBER: 2001-09-04
: PRIOR FILING DATE: 2000-04-06
: NUMBER OF SEQ ID NOS: 598
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 278
: LENGTH: 2470
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-822-849A-278

Query Match
Best Local Similarity 2.8%; Score 59.6; DB 10; Length 2470;
Matches 138; Conservative 0; Mismatches 104; Indels 6; Gaps 1;

QY 1588 TTCCACTTACCAGATGACCCCTCAATCCCATCATTAATGTGGTCCAGAAACCGGAT 1647
Db 1615 TTCCGCTGCTTCATCAGGCGACCAACGCGCTCATCATAGTGGGCCCCGACCGGGGTG 1674

QY 1648 GCGCCGTTTATGGGTTCTCTCAACATRAGAGAGAAATCTCAAGAACACACCCAGATGA 1707
Db 1675 GCACCCCTTCATATGGCTTCATCCAGAGAGGGGCTGGCTGCGACAGCAAGGCAAGGAGG- 1733

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RESULT 15
 US-09-938-842A-803
 Sequence 803: Application US/09938842A
 Patent No. US20020160378A1
 GENERAL INFORMATION:
 APPLICANT: Harper, Jeff
 APPLICANT: Kreps, Joel
 APPLICANT: Wang, Xun
 APPLICANT: Zhu, Tong
 TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 TITLE OF INVENTION: SAME, AND METHODS OF USE
 FILE REFERENCE: SCRIPT300-3
 CURRENT APPLICATION NUMBER: US/09/938, 842A
 CURRENT FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: US 60/227, 866
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: US 60/264, 647
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/300, 111
 PRIOR FILING DATE: 2001-06-22
 NUMBER OF SEQ ID NOS: 5379
 SEQ ID NO 803
 LENGTH: 2136
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-09-938-842A-803

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2003, 09:58:39 ; Search time 89.0595 Seconds

(without alignments)
7221.032 Million cell updates/sec

Title: US-09-371-347A-1

Perfect score: 2097
Sequence: 1 atgagagaggttctgttact.....ttcagatatattgtcataa 2097

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Issued_Patents_NA:*
- 2: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/6C_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2097	100.0	3259	4	US-09-318-448-23
2	386.4	18.4	390	4	US-08-905-223-71
3	63.6	3.0	4353	2	US-08-365-486A-18
4	63.6	3.0	4353	2	US-08-880-342-18
5	63.6	3.0	4780	2	US-08-365-486A-20
6	63.6	3.0	4780	3	US-09-123-708-3
7	63.6	3.0	4780	3	US-09-123-708-3
8	63.6	3.0	4780	4	US-08-880-342-20
9	57.2	2.7	5057	2	US-08-365-486A-12
10	57.2	2.7	5057	4	US-08-880-342-12
11	57.2	2.7	5108	4	US-07-642-002-1
12	53.6	2.6	1863	4	US-09-627-216A-13
13	52.8	2.5	1890	4	US-09-134-001C-1557
14	50.2	2.4	1448	4	US-08-302-620B-82
15	49.2	2.3	4145	4	US-09-302-620B-82
16	46.2	2.2	7218	4	US-08-232-463-14
17	46	2.2	4206	4	US-09-302-620B-81
18	44	2.1	307	4	US-09-172-711-24
19	43.4	2.1	7218	4	US-08-232-463-14
20	40.6	1.9	382	4	US-08-976-259-78
21	39.6	1.9	4041	4	US-08-147-812-4
22	39.6	1.9	4110	3	US-09-123-708-1
23	39.6	1.9	4110	3	US-09-123-708-1
24	39.6	1.9	4165	1	US-08-147-812-4
25	36.6	1.7	3701	1	US-08-553-279-1
26	36.6	1.7	45546	4	US-09-146-053-6
27	36	1.7	4089	1	US-07-908-245-1

28	36	1.7	4097	3	US-09-123-708-5	Sequence 5, App1
29	36	1.7	4097	3	US-09-123-708-5	Sequence 5, App1
30	35.4	1.7	1296	4	US-09-134-001C-1501	Sequence 1501, App1
31	34.2	1.6	1569	1	US-08-680-726A-57	Sequence 57, App1
32	34.2	1.6	1569	3	US-09-092-409-51	Sequence 51, App1
33	34.2	1.6	10592	1	US-08-680-726A-51	Sequence 51, App1
34	34.2	1.6	10592	1	US-08-680-726A-52	Sequence 52, App1
35	34.2	1.6	10592	3	US-09-092-409-51	Sequence 51, App1
36	34.2	1.6	10592	3	US-09-092-409-52	Sequence 52, App1
37	34	1.6	2223	3	US-08-257-073-4	Sequence 4, App1
38	33.8	1.6	1702	1	US-08-261-822A-14	Sequence 14, App1
39	33.8	1.6	1702	5	PCT-US95-07744A-14	Sequence 14, App1
40	33.8	1.6	4146	1	US-08-261-822A-15	Sequence 15, App1
41	33.8	1.6	4146	5	PCT-US95-07744A-15	Sequence 15, App1
42	33.2	1.6	2277	1	US-08-676-974-2	Sequence 2, App1
43	33.2	1.6	2277	1	US-08-676-974-2	Sequence 2, App1
44	33.2	1.6	2277	2	US-09-098-487-2	Sequence 2, App1
45	32.6	1.6	2193	4	US-09-427-261-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-09-318-448-23
; Sequence 23, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Steinhilber, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 3259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-23

Query Match 100.0%; Score 2097; DB 4; Length 3259;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAGGAGGTTTCTGTTACTATATGCTACACAGCAGGAGGACGCAAGGCCATCGCAGAA	60
DB	80	ATGAGGAGGTTTCTGTTACTATATGCTACACAGCAGGAGGACGCAAGGCCATCGCAGAA	139
QY	61	GAATGTGTCAGCAACTGTGGTACATGATTTTTCGACATCTTACATGATTAGTAA	120
DB	140	GAATGTGTCAGCAACTGTGGTACATGATTTTTCGACATCTTACATGATTAGTAA	199
QY	121	TTCGATAGATAGATACCTAAACCGAAACAGCTCTTGTGTGTTGTTTACACAG	180
DB	200	TTCGATAGATAGATACCTAAACCGAAACAGCTCTTGTGTGTTTACACAG	259
QY	181	GGCAGCGAGACCCAGCCAGCAGCAGCCGCAAGTTTGTAAAGAAATACAGAACCAAGA	240
DB	260	GGCAGCGAGACCCAGCCAGCAGCAGCCGCAAGTTTGTAAAGAAATACAGAACCAAGA	319
QY	241	CTGCGCGTTGATTTCTTCTCTACCTCGCGGTATAGGTTCTGCGTATTTAGAA	300
DB	320	CTGCGCGTTGATTTCTTCTCTACCTCGCGGTATAGGTTCTGCGTATTTAGAA	379
QY	301	TACACCTACTTTTGAATGGGGGAGATATATGATAACGACTTCAAGAGCTTGAGCC	360
DB	380	TACACCTACTTTTGAATGGGGGAGATATATGATAACGACTTCAAGAGCTTGAGCC	439
QY	361	CGGCAATTTCTATGACACTGAGACATGACATGACTGTAGGTTTGAACCTTGCTTGAG	420


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: TELEPHONE: (619) 235-8550
: TELEFAX: (619) 235-0176
: INFORMATION FOR SEQ ID NO: 71:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 390 base pairs
:   TYPE: NUCLEIC ACID
:   STRANDEDNESS: DOUBLE
:   TOPOLOGY: LINEAR
:   MOLECULE TYPE: cDNA
:   ORIGINAL SOURCE:
:     ORGANISM: Homo Sapiens
:     TISSUE TYPE: Brain
:   FEATURE:
:     NAME/KEY: sig.peptide
:     LOCATION: 288..357
:   IDENTIFICATION METHOD: Von Heijne matrix
:   OTHER INFORMATION: score 6.9
:   OTHER INFORMATION: seq SL5LASHSVSC/SN
US-08-905-223-71

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Query Match      18.4%: Score 386.4; DB 4; Length 390;
Best Local Similarity 99.7%: Pred. No. 2.1e-116;
Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 968 AGGTACAAAGCTTCTCAAGACTGCAGCTTGAAGATAAAGAGAGACGCTGCTCTT 1027
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DB 1 AAGTACAAAGCTTCTCAAGACTGCAGCTTGAAGATAAAGAGAGACGCTGCTCTT 60
OY 1028 TGAATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1087
    |||||
DB 61 TGAATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
OY 1088 GATGTTCTCCAGTTCATTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1147
    |||||
DB 121 GATGTTCTCCAGTTCATTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
OY 1148 CATTTTTCGAGGCTTGTGAGTATACAGTACAGTACAGTACAGTACAGTACAG 1207
    |||||
DB 181 CATTTTTCGAGGCTTGTGAGTATACAGTACAGTACAGTACAGTACAGTACAG 240
OY 1208 AGCTGTCACTAAACAAGGGGAGCGCATTAATAGCCGCTTTGATGAGATGCTGTGCT 1287
    |||||
DB 241 AGCTGTCACTAAACAAGGGGAGCGCATTAATAGCCGCTTTGATGAGATGCTGTGCT 300
OY 1268 GCTTGTGATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1327
    |||||
DB 301 GCTTGTGATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
OY 1328 AACATCTTCTTAACCTTCAACCCAGAGACC 1355
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DB 361 AACATCTTCTTAACCTTCAACCCAGAGACC 388

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RESULT 3
US-08-365-486a-18
: Sequence 18, Application US/08365486A
: Patent No. 5834306
: GENERAL INFORMATION:
:   APPLICANT: Webster, Keith A.
:   APPLICANT: Bishopric, Nanette H.
:   TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
:   TITLE OF INVENTION: Therapeutic Constructs
:   NUMBER OF SEQUENCES: 31
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Delinger & Associates
:     STREET: 350 Cambridge Avenue, Suite 250
:     CITY: Palo Alto
:     STATE: CA
:     COUNTRY: USA
:     ZIP: 94306
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible

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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/365,486A
:   FILING DATE: 23-DEC-1994
:   CLASSIFICATION: 514
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Sholtz, Charles K.
:     REGISTRATION NUMBER: 38,615
:     TELECOMMUNICATION INFORMATION:
:       TELEPHONE: (415) 324-0880
:       TELEFAX: (415) 324-0960
:   INFORMATION FOR SEQ ID NO: 18:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 4353 base pairs
:     TYPE: nucleic acid
:     STRANDEDNESS: double
:     TOPOLOGY: Linear
:     MOLECULE TYPE: cDNA to mRNA
:     HYPOTHETICAL: NO
:     ANTI-SENSE: NO
:     ORIGINAL SOURCE:
:       INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al.
:       INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
:   FEATURE:
:     NAME/KEY: CDS
:     LOCATION: 1..4305
US-08-365-486a-18

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Query Match      3.0%: Score 63.6; DB 2; Length 4353;
Best Local Similarity 48.8%: Pred. No. 5.6e-10;
Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

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OY 1588 TTCACCTTACCAATGACCCCTCAATCCCAATCAATGATGATGATGATGATGAT 1647
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DB 3715 TTCACCTTACCAATGACCCCAATCCCAATGATGATGATGATGATGATGATGAT 3774
OY 1648 GCGCCGCTTATGCTGCTCTCAACATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1707
    |||||
DB 3775 GCGCCGCTTATGCTGCTCTCAACATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3831
OY 1708 AATTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1767
    |||||
DB 3832 AAGCCCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3891
OY 1768 AGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1827
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DB 3892 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3951
OY 1828 TCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1887
    |||||
DB 3952 TCCC-----GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3996
OY 1888 GAGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1947
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DB 3997 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4056
OY 1948 TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2007
    |||||
DB 4057 GTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4116
OY 2008 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2067
    |||||
DB 4117 CAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4176
OY 2068 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2089
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DB 4177 AAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTT 4198

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RESULT 4
US-08-880-342-18

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Sequence 18, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4353 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al,
INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4305
US-08-880-342-18

Query Match 3.0%; Score 63.6; DB 4; Length 4353;
Best Local Similarity 48.8%; Pred. No. 5.6e-10;
Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

QY 1588 TTCACATTACAGATGACCCCTGATCCCATATATGTTGGTCCAGGACCGGATG 1647
DB 3715 TTCACACTGCGCCGGAACCCCAAGTCCCTGCATCCTGTTGGACGACGACGGCAT 3774
QY 1648 GCCCGCTTTATTTGGTTCTTACACATAGAGAGAACTCCAAAGAACACCCAGATGA 1707
DB 3775 GCCCGCTTTCCGAAGCTTCTGGCAACAGCG--GCAATTGATATCCAAAGGATG 3831
QY 1708 AATTTGGAGCAATGAGTGTGTTTGGCTGAGCATAGATAGGATATTCATTC 1767
DB 3832 AACCCCTGCCCCATGCTGCTGCTGGGTGCGGCAATCAAGATGATATCTTAC 3891

QY 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATGAAGGTTTCCCTTC 1827
DB 3892 AGGAGAGACACCTGCGAGGCCAAGAACAGAGGGGTCTTTCAGAGCTGTACACGGCTTAC 3951
QY 1828 TCAAGAGATCTCTCTGTTGGGAGAGGAAAGCCCAAGCAAGTATGATCAAGCAACATC 1887
DB 3952 TCCC-----GGAGCCAGACAAACCAAGAAATGATGCGAGGACATTCCTG 3996
QY 1888 CAGCTTCATGCGCAGCAGAGTGGGAGAGATCTCTCTCCAGAGAAAGGCCATATTATGTG 1947
DB 3997 CAGAGCAGCTGCGGAGCTGTGTACCGAGCCCTGAAGAGCAAGGGGCCACATATAC 4056
QY 1948 TGTGAGATGCAAAAGATATGCGCAAGAGATGATGCTCTGTGCAAAATATATACG 2007
DB 4057 GTCTGTGGGAGACGTCACCATGCTGCTGATGCTCTCAAGCCATCCAGCCGATCATGACC 4116
QY 2008 AAAGAGTTGAGCTTGAANAAGTAAAGCAATGAANAACCTGSCCATTTAAAGAGAA 2067
DB 4117 CAGCAGGGGAAGCTCTCGCAGAGACGCCGCGTATTCATCAGCCGATGAGGATGAC 4176
QY 2068 AAACGCTACCTGAGATATT 2089
DB 4177 AACGATACCATGAGATATT 4198

RESULT 5
US-08-365-486A-20
Sequence 20, Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 4780 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human NOS-1N gene, Nakane, et al,
INDIVIDUAL ISOLATE: FEBS Lett 316:175 (1993)
FEATURE:
NAME/KEY: CDS
LOCATION: 431..4732

Db	4259	AAACCCTGCCCCAGTCTGGTCTTGCGGGTCCGGCAATCCAGATGATCATATCTAC	4318
QY	1768	AGAAAAGAGCTCAGACATTTTCTTAAAGCATGGATCTTAACTCATCTTAAAGTTTCTTC	1827
Db	4319	AGGGAGAGACCTTCGACGGCCAGAACACAAAGGGCTCTTCAAGAGAGCTGTACACGGCTTAC	4378
QY	1828	TCAAGAGATGCTCTGTGTTGGGAGAGGAAACCCACGAAAGTATGTATCAAGACACATC	1887
Db	4379	TCCC-----GGAGCCAGACAAACCCAAAGATGTCGTACAGACATCTG	4423
QY	1888	CAGCTTCATGGCCACGAGGTGGCCAGATCTCTCCACGAGAAACGGCCATATTATGTG	1947
Db	4424	CAGGAGCAGCTGGGGAGTCTGTATCCAGACCTTGAAGAGGCAAGGGGGCCACATATAC	4483
QY	1948	TGTGAGATGTCAAAGAAATATGGCCAAAGATGTACATGATGCCCTTGTGTCAATAATAAGC	2007
Db	4484	GTCGTGTGGGGAGCTCACCATGTGCTGTGATGTCTCTCAAGGCCATTCAGCGCATATGACC	4543
QY	2008	AAAGAGTTGGAGTTGAAAACTTGAAGCAATGAAAACTTGCCACTTTTAAAGAAAGAA	2067
Db	4544	CAGCAGGGGAAGCTCTCGGCGAGAGAGCGCGGCTATTATTCACACCGGATGAGGGATGAC	4603
QY	2068	AAACGCTACCTTCAGATATT	2089
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? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? INDIVIDUAL ISOLATE: Human NOS-5N gene, Nakane, et al
? INDIVIDUAL ISOLATE: FEBS Lett 316:175 (1993)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 431..4732
? US-08-880-342-20

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SRO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: rat bnos cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 349..4638
US-08-365-486A-12
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Query Match      2.7%; Score 57.2; DB 2; Length 5057;
Best Local Similarity 48.0%; Pred. No. 7.8e-08;
Matches 241; Conservative 0; Mismatches 243; Indels 18; Gaps 2;
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DB 4048 TTCGACTTACAGATGACCCCTCATATCCATATATGTTGGTCCAGAACCGGATA 4107
OY 1648 GCGCCGTTTATGGGTTCTTACACATAGAGAACTCCAAAGAACACCCGATGGA 1707
    || ||| ||| ||||| ||| ||| ||||| ||||| |||||
DB 4108 GCACCTTCCGAAGCTTCTGCGACACGAC---AATTTGACATCCAAAGAAATG 4164
OY 1708 AATTTTGAGCAATGTGTTGTTTGGCTGCAGCATTAAGATATGATATCTATTC 1767
    ||| ||| ||| ||||| ||| ||| ||||| ||||| |||||
DB 4165 AATCGTGCCCAATGTTCTGTGTTCTGGGTGTGACAAATCCAAAGATATGATCTAC 4224
OY 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAACTCATCTAAAGTTCTTC 1827
    ||| ||| ||| ||||| ||| ||| ||||| ||||| |||||
DB 4225 AGAGAGGAGACCTTGCGAGCTAAGAACAGGGCGTCTTCAAGAGCTGTACACTGCCTAT 4284
OY 1828 TCAAGAGATGCTCTCTGTTGGGAGAGGAAGCCCAAGATATGTACAAAGACATC 1887
    || ||| ||| ||||| ||| ||| ||||| ||||| |||||
DB 4285 TCCCGGGAACC-----GGACAGGCCAAAGAAATATGTACAGACGTGCTG 4329
OY 1888 CAGCTTCATGCGCCAGCATGTCGAGAAATCTCTCCAGAGAAAGCCCATATTTATGTG 1947
    ||||| ||| ||||| ||| ||| ||||| ||||| |||||
DB 4330 CAGGACAGCTGGCTGTGCTGTGTACCGGCGCTGAAGAGGAAAGAGGCGACATTTAT 4389
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OY 2008 AAAGAGGTTGAGTTGAAAACTAAGCAATGAAACCTTGCGCACTTTAAAGAAAGAA 2067
    ||||| ||| ||||| ||| ||| ||||| ||||| |||||
DB 4450 CAGAGAGGGAACCTCTAGAGAGGAGACGTGTGTATTTATCATCAGCAGGCTGAGGATGAC 4509
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DB 4510 AACCGGTACCAAGAGACATCT 4531
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RESULT 10
US-08-880-342-12

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Sequence 12, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SRO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: rat bnos cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 349..4638
US-08-880-342-12
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Query Match 2.7%; Score 57.2; DB 4; Length 5057;

Best Local Similarity 48.0%; Pred. No. 7.8e-08;

Matches 241; Conservative 0; Mismatches 243; Indels 18; Gaps 2;

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OY 1588 TTCGACTTACAGATGACCCCTCATATCCATATATGTTGGTCCAGAACCGGATA 1647
    ||||| ||| ||||| ||| ||| ||||| ||||| |||||
DB 4048 TTCGACTTACAGATGACCCCTCATATCCATATATGTTGGTCCAGAACCGGATA 4107
OY 1648 GCGCCGTTTATGGGTTCTTACACATAGAGAACTCCAAAGAACACCCGATGGA 1707
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DB 4108 GCACCTTCCGAAGCTTCTGCGACACGAC---AATTTGACATCCAAAGAAATG 4164
OY 1708 AATTTTGAGCAATGTGTTGTTTGGCTGCAGCATTAAGATATGATATCTATTC 1767
    ||| ||| ||| ||||| ||| ||| ||||| ||||| |||||
DB 4165 AATCGTGCCCAATGTTCTGTGTTCTGGGTGTGACAAATCCAAAGATATGATCTAC 4224
OY 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAACTCATCTAAAGTTCTTC 1827
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Db	4225	AGAGAGGAGACCTTCGACGGCTAAGAACACAGGGCGCTTCCANAGAGCTGTACACGTCCAT	4284
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Db	4285	TCCCGGGGAAC-----GGACAGGCCAAAGAAATATGTACAGAGCGTCTG	4329
QY	1888	CAGCTTATGAGCCAGCAGGTGGCAGAGATCCTTCCTCCAGGAGAACGGGCATATTTATGTG	1947
Db	4330	CAGGAACAGCTGGCTGTAGTCTGTGTACCGCGCCCTGGAAGGAGCAAGGAGGCCACATTTAT	4389
QY	1948	TGTGGAATGTCAAAGAAATATGGCCAGAGATGTACATGATGCCCTTGTGCCAATAATAAGC	2007
Db	4390	GTCGTGTGGGGACGTTACCATTGGCCGCGATGTCTCTCAAGAGCATCCAGCGCATATATGACC	4449
QY	2008	AAAAGGTTGGAGTTGAAAAACTGAAAGCAATGAAAAACCCTGGCCACTTTTAAAAAGAA	2067
Db	4450	CAGCAGGGGGAACCTCTCAGAGGAGACGCTGGTATTATTCATCAGCAGAGCTGAGGGATGAC	4509
QY	2068	AAACGTAACCTTCAGGATATTT	2089
Db	4510	AACCGGTACCCAGAGGACATCT	4531

RESULT 11
 US-07-642-002-1
 Sequence 1, Application US/07642002
 Patent No. 5268465
 GENERAL INFORMATION:
 APPLICANT: Bredt, David S.
 APPLICANT: Hwang, Paul M.
 APPLICANT: Reed, Randall
 APPLICANT: Snyder, Solomon H.
 TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
 TITLE OF INVENTION: Oxide Synthase
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Banner Birch, McKie & Beckett
 STREET: One Thomas Circle, NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/642,002
 FILING DATE: 19910118
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kagan, Sarah A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 1107.033576
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 296-5500
 TELEFAX: (202) 296-7830
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5108 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: N
 ANTI-SENSE: N
 ORIGINAL SOURCE:
 ORGANISM: Rattus rattus
 TISSUE TYPE: Brain
 FEATURE:
 NAME/KEY: CDS

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; LOCATION: 400..4686
; OTHER INFORMATION:
US-07-642-002-1

Query Match	2.7%	Score 57.2;	DB 1;	Length 5108;
Best Local Similarity	48.0%	Pred. No. 7.9e-08;		
Matches 241;	Conservative	0;	Mismatches 243;	Indels 18; Gaps 2;

QY	1588	TTTCACTTACAGATGACGACCCCTCAATCCATCCATCTCAATGATGGGGTCCAGAGAACCGGATA	1647
Dd	4099	TTTCACTTACAGATGACGACCCCTCAATCCATCCATCTCAATGATGGGGTCCAGAGAACCGGATA	4158
QY	1648	GCCCCGTTTATTTGGGTTCTTCAACATAGAGAGAACTCCAAGAACACACCCAGATGA	1707
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QY	1708	AATTTTGGAGCAATGTGGTGTGTTTGGCTGCGACGCAATAGGATPAGGATTAATCTATTC	1767
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QY	1828	TCAAGAGATGCTCCTGTTGGGGAGAGAGAACCCGACCAAGTATGTATCAAGACACATC	1887
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Dd	4381	CAGGAACAGCTGGGTGATGTGTGTACCGGCCCTGAAAGGAGCAAGAGGCGCACATTTAT	4440
QY	1948	TGTGGAGATGCAAAAGATATGTGCCCAAGAGTATACATGATGCCCTTTGGCAATATTAAG	2007
Dd	4441	GTCTGTGGGCGATTACCATGGCGCGCGATGCTCTCAAGGCACTACAGCGCATATATAC	4500
QY	2008	AAAGAGGTTGAGTGTGAAAACTAGAAAGATGAAACCCCTGGCCACTTTAAAGAGAA	2067
Dd	4501	CAGCAGGGGAATCTCTGAGAGAGAGAGCGTGTATTTCAATCAGCAGGCTGAGGGATGAC	4560
QY	2068	AAAGCTTACCTTCAGATATTT	2089
Dd	4561	AACGGTATCCAGAGGACATCT	4582

RESULT 12

US-09-627-216A-13
; Sequence 13, Application US/09627216A

; Patent No. 6368837
; GENERAL INFORMATION:

; APPLICANT: Sariaslani, Sima F
; APPLICANT: Tang, Xiao-Song

; APPLICANT: Qi, Wei Wei.
 ; APPLICANT: Vannelli, Todd

;; APPLICANT: Gatenby, Anthony
;; TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid

FILE REFERENCE: BC1009 US NA
CURRENT APPLICATION NUMBER: US/09/627,216A

;; CURRENT FILING DATE: 2000-07-27
;; PRIOR APPLICATION NUMBER: 60/147,719

;; PRIOR FILING DATE: 1999-08-06
;; NUMBER OF SEQ ID NOS: 14

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; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
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; LENGTH: 1863
; TYPE: DNA

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ORGANISM: Helianthus tuberosus
US-09-627-216A-13

Query Match	2.6%;	Score 53.6;	DB 4;	Length 1863;
Best Local Similarity	48.8%;	Pred. No. 6e-07;		
Matches 254;	Conservative 0;	Mismatches 239;	Indels 27;	Gaps 3;

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	Best Local Similarity	49.2%:	Pred. No. 1.le-06:		
	Matches 258:	Conservative	0:	Mismatches 227:	Indels 39; Gaps 3;
OY	1554	TAAGTATCCACTCTCCTCGAACAACAAATTTTTCACATTACAGATGACCCTCAT	1613		
Db	1389	TACAATTCCTATCTATTAAAAACGAATCCGAATTTTAAGTTTTCCGCAAGATGATCAAC	1448		
OY	1614	CCCCATCATATGGTGSGSTCCAGAACCGCATAGCCCCGTTTATATGGGTCCTACACAA	1673		
Db	1449	ACCGTGTATTATGATAGGCTCCTGGACACGGGTGTGCACCGTTTAAATCCTATATGACAAGA	1508		
OY	1674	TAGAGAGAACTCCAAGAACAAACCCAGATGGAATTTTGGAGCAATGTGTGTTTTT	1733		

Db	1509	ACGAGAGGAACTA-----GGTTTGAAGCAAAATACATGGTTATCTT	1550
Qy	1734	TGCGTCGACGCATTAAGGATAGGATTATCTATTCAGAAAAGAGCTCAGACATTTCTTAA	1793
Db	1551	TGGAGATCAACACTTCACTACAGATTTTCTGTATCAACAGGAATGGCAAGATGCGTTGA	1610
Qy	1794	GCATGGGATCTTAACTCATCTTAAAGGTTTCTTCTCAAGAGATGCTCTGTGGGGAGGA	1853
Db	1611	AGATGGGAACCTTATCAAAAATTAGATGTTGCTTTTCTTAGAGA---TACTGTATAAAAAGT	1667
Qy	1854	GGAAGCCCCAGCAAAATGTATGACAAAGACAAACATCCAGCTTATGCGCCAGCGATGGCGAG	1913
Db	1668	GTAATGTCACACATATAATTTAGTGAATAATAGTGAAACATTTTAATGATG-----	1716
Qy	1914	AATCCCTCCAGGAGAAAGCGCCATATTTATGTGTGTGGAGATGCMAAAGATATGGCCAA	1973
Db	1717	-----ATTGAAAATGGCGCGCTACTACTATTATGTATGTGTGATGAAAGTAAATAATCGAAA	1769
Qy	1974	GGATGTACATATATGCCCTTGTGTCAAAATTAATAAGCAAAAGAGTTGGAGTTGAAAAACTGA	2033
Db	1770	GGAGTGTTCATCAAGCGATTAAAAATATGCTTTAATCAAAAGAGCAAAAACCTATCTGAAACAGA	1829
Qy	2034	AGCATGAAAACCCGTGGCCACTTTAAAGAAGAAAAAGCTTACC	2077
Db	1830	TGCAGAGAAATACTTTAAACAATGAAGAAAGATTAAGATATTC	1873

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: RESULT 14
: US-08-936-165A-113
: Sequence 113: Application US/08936165A
: Patent No. 6348582
: GENERAL INFORMATION:
: APPLICANT: Black, Michael
: APPLICANT: Burnham, Martin
: APPLICANT: Hodgson, John
: APPLICANT: Knowles, David
: APPLICANT: Lonetto, Michael
: APPLICANT: Nicholas, Richard
: APPLICANT: Pratt, Julie
: APPLICANT: Reichard, Richard
: APPLICANT: Rosenberg, Martin
: APPLICANT: Ward, Judith
: TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides
: TITLE OF INVENTION: Polypeptides and Their Uses
: NUMBER OF SEQUENCES: 534
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406-0939
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/936,165A
: FILING DATE: 24-SEP-1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/027,032
: FILING DATE: 24-SEP-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Gimm, Edward R
: REGISTRATION NUMBER: 38,891
: REFERENCE/DOCKET NUMBER: P50549
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-4478
: TELEFAX: 610-270-5090
: TEXT:
: INFORMATION FOR SEQ ID NO: 113:

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GenCore version 5.1.6
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(without alignments)
239.574 Million cell updates/sec

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Perfect score: 109
Sequence: 1 GAMWIFGCRHKRDYLF 18

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Searched: 1439767 seqs, 1031500376 residues
Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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Published Applications_NA.*
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16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	109	100.0	2097	12	US-09-371-347-1	Sequence 1, Appl1
3	109	100.0	2097	12	US-09-371-347-41	Sequence 41, Appl
4	109	100.0	2097	12	US-09-371-347-43	Sequence 43, Appl
5	109	100.0	3259	12	US-09-371-347-24	Sequence 24, Appl
6	94.5	86.7	2094	11	US-09-371-347-45	Sequence 45, Appl
7	76	69.7	101	11	US-09-783-590-1364	Sequence 1364, Ap
8	60	55.0	315	8	US-08-781-986A-941	Sequence 941, App
9	60	55.0	3690	11	US-09-870-759-123	Sequence 123, App
10	60	55.0	13508	8	US-08-781-986A-120	Sequence 120, App
11	59	54.1	230	10	US-09-923-876-2845	Sequence 2845, Ap
12	59	54.1	298	10	US-09-294-093B-4842	Sequence 4842, Ap
13	58	53.2	1872	11	US-09-917-800A-1351	Sequence 1351, Ap
14	58	53.2	2401	11	US-09-917-800A-1397	Sequence 1397, Ap
15	58	53.2	2403	11	US-09-880-107-3039	Sequence 3039, Ap
16	58	53.2	2470	10	US-09-822-849A-278	Sequence 278, App
17	57	52.3	1845	15	US-10-128-714-1234	Sequence 1234, Ap
18	57	52.3	1845	15	US-10-128-714-2234	Sequence 2234, Ap
19	57	52.3	2088	15	US-10-128-714-7234	Sequence 7234, Ap
20	57	52.3	2145	15	US-10-128-714-6234	Sequence 6234, Ap
21	57	52.3	3845	15	US-10-128-714-5234	Sequence 5234, Ap
22	57	52.3	4145	15	US-10-128-714-8234	Sequence 8234, Ap
23	56	51.4	367	11	US-09-867-701-1581	Sequence 1581, Ap
24	55	50.5	491	11	US-09-974-300-6448	Sequence 6448, Ap
25	55	50.5	3855	15	US-10-210-682-1	Sequence 1, Appl1
26	54	49.5	555	11	US-09-974-300-6632	Sequence 6632, Ap
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28	53	48.6	1791	11	US-09-778-319-1	Sequence 1, Appl1
29	53	48.6	1944	15	US-10-272-017A-1	Sequence 1, Appl1
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31	53	48.6	3037	10	US-09-911-781-10	Sequence 10, Appl
32	53	48.6	3219	15	US-10-156-761-567	Sequence 567, Appl
33	53	48.6	4145	10	US-09-911-781-3	Sequence 3, Appl1
34	53	48.6	4145	12	US-09-976-800-82	Sequence 82, Appl
35	53	48.6	4145	15	US-10-138-838-82	Sequence 82, Appl
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37	53	48.6	4145	15	US-10-138-905-82	Sequence 82, Appl
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39	53	48.6	4206	10	US-09-911-781-2	Sequence 2, Appl1
40	53	48.6	4206	12	US-09-976-800-81	Sequence 81, Appl1
41	53	48.6	4206	15	US-10-138-838-81	Sequence 81, Appl
42	53	48.6	4206	15	US-10-138-905-81	Sequence 81, Appl
43	53	48.6	4206	15	US-10-138-905-81	Sequence 81, Appl
44	53	48.6	4206	15	US-10-138-916-81	Sequence 81, Appl
45	53	48.6	9025608	15	US-10-156-761-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-371-347-47
; Sequence 47, Application US/09371347
; Publication No. US20030082676A1

GENERAL INFORMATION:

APPLICANT: Roy A. Gravel et al.
TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;
TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371,347
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/071,622
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/232,028
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 47
LENGTH: 2093
TYPE: DNA

ORGANISM: Homo sapiens

Alignment Scores:

```
Pred. No.: 3.6e-09 Length: 2093
Score: 109.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-371-347A-25 (1-18) x US-09-371-347-47 (1-2093)

QY 1 G1yAlaMetTpLeuPhpHeG1yCysArgh1sLysAspArgAspTyrLeuPhe 18
Db 1714 GGAGCAATGTGTTCTTTTGGCTGCAGCATAGGATTATCTATTC 1763

RESULT 2
US-09-371-347-1
; Sequence 1, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-1

Alignment Scores:
Pred. No.: 3.61e-09 Length: 2097
Score: 109.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-371-347A-25 (1-18) x US-09-371-347-1 (1-2097)

QY 1 G1yAlaMetTpLeuPhpHeG1yCysArgh1sLysAspArgAspTyrLeuPhe 18
Db 1714 GGAGCAATGTGTTCTTTTGGCTGCAGCATAGGATTATCTATTC 1767

RESULT 3
US-09-371-347-41
; Sequence 41, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-09-371-347-41

Alignment Scores:
Pred. No.: 3.61e-09 Length: 2097
Score: 109.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-371-347A-25 (1-18) x US-09-371-347-41 (1-2097)

QY 1 G1yAlaMetTpLeuPhpHeG1yCysArgh1sLysAspArgAspTyrLeuPhe 18
Db 1714 GGAGCAATGTGTTCTTTTGGCTGCAGCATAGGATTATCTATTC 1767

RESULT 4
US-09-371-347-43
; Sequence 43, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-43

Alignment Scores:
Pred. No.: 3.61e-09 Length: 2097
Score: 109.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-371-347A-25 (1-18) x US-09-371-347-43 (1-2097)

QY 1 G1yAlaMetTpLeuPhpHeG1yCysArgh1sLysAspArgAspTyrLeuPhe 18
Db 1714 GGAGCAATGTGTTCTTTTGGCTGCAGCATAGGATTATCTATTC 1767

RESULT 5
US-09-371-347-24
; Sequence 24, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
```

```
; LENGTH: 3259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-24

Alignment Scores:
Pred. No.: 6,01e-09      Length: 3259
Score: 109.00           Matches: 18
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 12                  Gaps: 0

US-09-371-347a-25 (1-18) x US-09-371-347-24 (1-3259)

QY 1 GAlaMetTrPLeuphepGhGlyCysArghIstLysAspArgAspTyrLeuphe 18
    |||||||
DB 1793 GGAGCAATGTGTGTTTGGCTGCAGCATAGATAGGATTATCTATTC 1846

RESULT 6
US-09-371-347-45
; Sequence 45, Application US/09371347
; Publication No. US20030082676a1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371.347
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-45

Alignment Scores:
Pred. No.: 1.19e-06      Length: 2094
Score: 94.50            Matches: 17
Percent Similarity: 94.44%  Conservative: 0
Best Local Similarity: 94.44%  Mismatches: 0
Query Match: 86.70%      Indels: 1
DB: 12                  Gaps: 1

US-09-371-347a-25 (1-18) x US-09-371-347-45 (1-2094)

QY 1 GAlaMetTrPLeuphepGhGlyCysArghIstLysAspArgAspTyrLeuphe 18
    |||||||
DB 1714 GGAGCAATGTG---TTTGGCTGCAGCATAGATAGGATTATCTATTC 1764

RESULT 7
US-09-783-590-1364
; Sequence 1364, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
```

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; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1364
; LENGTH: 101
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (62)
; OTHER INFORMATION:
US-09-783-590-1364

Alignment Scores:
Pred. No.: 5.81e-05      Length: 101
Score: 76.00            Matches: 15
Percent Similarity: 84.21%  Conservative: 1
Best Local Similarity: 78.95%  Mismatches: 2
Query Match: 69.72%      Indels: 1
DB: 11                  Gaps: 0

US-09-371-347a-25 (1-18) x US-09-783-590-1364 (1-101)

QY 1 GAlaMetTrPLeuphepGhGlyCysArghIstLysAspArgAspTyrLeuphe 18
    |||||||
DB 42 GGAGCAATGTGTGTTTGGCTGCAGCATAGGATTAGGATTATCTATTC 96

RESULT 8
US-08-781-986a-941
; Sequence 941, Application US/08781986A
; Publication No. US2003005436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5555
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248BP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 941:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986a-941
```

Alignment Scores:

Pred. No.:	0.13	Length:	315
Score:	60.00	Matches:	9
Percent Similarity:	72.22%	Conservative:	4
Best Local Similarity:	50.00%	Mismatches:	5
Query Match:	55.05%	Indels:	0
DB:	8	Gaps:	0

US-09-371-347a-25 (1-18) x US-08-781-986a-941 (1-315)

Oy 1 GLYALAMETTRPLEUPHEPHEGLYCYSARGHISLYSASPARGASPTYRLEUPHE 18
Db 146 GGAATAACATGCTGTCTTTGTTGGTGCACACCGCTAGCTTCTGACTTTTATAT 199

RESULT 9

US-09-870-759-123

Sequence 123, Application US/09870759

Patent No. US20020177551A1

GENERAL INFORMATION:

APPLICANT: TERMAN, David S

FILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REFERENCE: 870759

CURRENT APPLICATION NUMBER: US/09/870,759

PRIOR FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: US 60/208,128

PRIOR FILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 166

SOFTWARE: PatentIn version 3.1

SEQ ID NO 123

LENGTH: 3690

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: CDS

LOCATION: (256)..(3690)

OTHER INFORMATION:

US-09-870-759-123

Alignment Scores:

Pred. No.:	2.23	Length:	3690
Score:	60.00	Matches:	10
Percent Similarity:	72.22%	Conservative:	3
Best Local Similarity:	55.56%	Mismatches:	5
Query Match:	55.05%	Indels:	0
DB:	11	Gaps:	0

US-09-371-347a-25 (1-18) x US-09-870-759-123 (1-3690)

Oy 1 GLYALAMETTRPLEUPHEPHEGLYCYSARGHISLYSASPARGASPTYRLEUPHE 18
Db 3259 GCGCGCATGAGCTGTGTGTTGGTGGCGCACCCGAGGAGGACACCTCTAT 3312

RESULT 10

US-08-781-986a-120

Sequence 120, Application US/08781986A

Publication No. US20030054436A1

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8512

TELEFAX: (301) 309-8504

INFORMATION FOR SEQ ID NO: 120:

SEQUENCE CHARACTERISTICS:

LENGTH: 13508 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-781-986a-120

Alignment Scores:

Pred. No.:	9.99	Length:	13508
Score:	60.00	Matches:	9
Percent Similarity:	72.22%	Conservative:	4
Best Local Similarity:	50.00%	Mismatches:	5
Query Match:	55.05%	Indels:	0
DB:	8	Gaps:	0

US-09-371-347a-25 (1-18) x US-08-781-986a-120 (1-13508)

Oy 1 GLYALAMETTRPLEUPHEPHEGLYCYSARGHISLYSASPARGASPTYRLEUPHE 18
Db 1236 GGAATAACATGCTGTCTTTGTTGGTGCATCACACCGTACTGCTCTTTATAT 1289

RESULT 11

US-09-923-876-2845

Sequence 2845, Application US/09923876

Patent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Laligudi, Raghunath V.

APPLICANT: Kamigaki, Laura Y. (Itc)

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876

CURRENT FILING DATE: 2001-08-06

PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: 60/085,331

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL Program

SEQ ID NO 2845

LENGTH: 230

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: misc-feature

OTHER INFORMATION: Incyte ID No. US20020013958A1 700161271H1

NAME/KEY: unsure

LOCATION: 196

OTHER INFORMATION: a, t, c, g, or other

US-09-923-876-2845

Alignment Scores:

Pred. No.:	0.134	Length:	230
Score:	59.00	Matches:	9
Percent Similarity:	77.78%	Conservative:	5
Best Local Similarity:	50.00%	Mismatches:	4
Query Match:	54.13%	Indels:	0
DB:	10	Gaps:	0

Pred. No.: 3.02 Length: 2401
Score: 58.00 Matches: 9
Percent Similarity: 66.67% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 53.21% Indels: 0
DB: 11 Gaps: 0

US-09-371-347A-25 (1-18) x US-09-917-800A-1397 (1-2401)

QY 1 GYAlaMetTrpLeuPheGlyCysArgHisLysAspArgAspTyrLeuPhe 18
DB 1676 GGAGAGACCGCTGCTACTATGCGCTCCGCGCTCGATGAGGACTATCTGTAC 1729

RESULT 15

US-09-880-107-3039.
; Sequence 3039, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3039
; LENGTH: 2403
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 S90469
US-09-880-107-3039

Alignment Scores:

Pred. No.:	3.02	Length:	2403
Score:	58.00	Matches:	9
Percent Similarity:	66.67%	Conservative:	3
Best Local Similarity:	50.00%	Mismatches:	6
Query Match:	53.21%	Indels:	0
DB:	11	Gaps:	0

US-09-371-347A-25 (1-18) x US-09-880-107-3039 (1-2403)

QY 1 GYAlaMetTrpLeuPheGlyCysArgHisLysAspArgAspTyrLeuPhe 18
DB 1669 GGGAGACGCTGCTACTACTACGCGCTCGCGCTCGATGAGGACTACTCTGTAC 1722

Search completed: July 29, 2003, 13:11:26
Job time : 163 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: July 29, 2003, 12:57:24 ; Search time 39 Seconds
(without alignments)
141.543 Million cell updates/sec

Title: US-09-371-347A-25

Perfect score: 109
Sequence: 1 GAWMLFFGCRHKKDRDYLF 18

Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued Patents_NA:*

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- 2: /cg2n2_6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cg2n2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cg2n2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cg2n2_6/ptodata/1/ina/CTUS.COMB.seq:*
- 6: /cg2n2_6/ptodata/1/ina/backfiles1.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	3259	4	US-09-318-448-23
2	60	55.0	4041	1	US-08-147-812-4
3	60	55.0	4110	3	US-09-123-708-1
4	60	55.0	4110	3	US-09-123-708-1
5	60	55.0	4110	3	US-09-123-708-1
6	58	53.2	3701	1	US-08-147-812-6
7	55	50.5	4062	4	US-09-126-109-11
8	55	50.5	4145	1	US-08-314-917-1
9	55	50.5	4145	1	US-08-265-046-1
10	55	50.5	4145	2	US-08-465-522-1
11	55	50.5	4145	5	PCT-US93-11401-1
12	55	50.5	4145	5	PCT-US95-07849-1

13	53	48.6	1890	4	US-09-134-001C-1557	Sequence 1557, Ap
14	53	48.6	4145	4	US-09-302-620B-82	Sequence 82, Appl
15	53	48.6	4206	4	US-09-302-620B-81	Sequence 81, Appl
16	51	46.8	4816	1	US-08-592-214A-22	Sequence 22, Appl
17	51	46.8	4816	3	US-09-149-976-22	Sequence 22, Appl
18	50	45.9	1863	4	US-09-627-216A-13	Sequence 13, Appl
19	48	44.0	382	4	US-08-976-259-78	Sequence 78, Appl
20	46	42.2	3215	1	US-08-426-627-1	Sequence 280, App
21	45	41.3	467	1	US-08-474-542A-780	Sequence 280, App
22	45	41.3	467	1	US-08-457-648-280	Sequence 280, App
23	45	41.3	1776	4	US-09-149-476-59	Sequence 59, Appl
24	45	41.3	1791	4	US-09-149-476-226	Sequence 226, App
25	45	41.3	4615	2	US-08-674-351-3	Sequence 3, Appl1
26	45	41.3	5183	2	US-08-870-518-7	Sequence 7, Appl1
27	44.5	40.8	72604	4	US-09-268-997-7	Sequence 7, Appl1
28	44.5	40.8	72604	4	US-09-657-474-7	Sequence 7, Appl1
29	44	40.4	4724	4	US-09-066-046-3	Sequence 3, Appl1
30	44	40.4	4825	6	5459251-1	Sequence 3, Appl1
31	44	40.4	5086	2	US-08-465-485A-19	Sequence 19, Appl
32	44	40.4	5086	2	US-08-365-486A-14	Sequence 14, Appl
33	44	40.4	5086	3	US-09-080-285-19	Sequence 19, Appl
34	44	40.4	5086	4	US-08-880-342-14	Sequence 14, Appl
35	44	40.4	5086	4	US-09-724-426-19	Sequence 19, Appl
36	44	40.4	5086	4	US-09-233-527-7	Sequence 7, Appl1
37	44	40.4	5086	5	PCT-US93-05651-4	Sequence 4, Appl1
38	44	40.4	5086	5	PCT-US93-06251-2	Sequence 2, Appl1
39	44	40.4	5094	4	US-09-234-186-7	Sequence 7, Appl1
40	44	40.4	5104	6	5506344-1	Sequence 7, Appl1
41	44	40.4	6416	4	US-09-136-574A-2	Sequence 2, Appl1
42	44	40.4	6736	3	US-09-057-570-1	Sequence 1, Appl1
43	44	40.4	6736	3	US-09-057-570-5	Sequence 5, Appl1
44	44	40.4	7004	3	US-09-057-570-3	Sequence 3, Appl1
45	43.5	39.9	1960	2	US-08-463-081B-9	Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-09-318-448-23
Sequence 23, Application US/09318448
Patent No. 6210950
GENERAL INFORMATION:
APPLICANT: Johnson, William G.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
FILE REFERENCE: 601-1-057
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 3259
TYPE: DNA
ORGANISM: Homo sapiens
US-09-318-448-23

Alignment Scores:
Pred. No.: 1.8e-09
Score: 109.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0

US-09-371-347A-25 (1-18) x US-09-318-448-23 (1-3259)

OY 1 GYALAMEVTPLEUPHepheGlyCysArgHISLysAspArgAspTYLeuPhe 18
DB 1793 GGAGCAATGCTGTTTGTTCGCTGCAGCGCAATAAGATAGGATATCTATTTC 1846
RESULT 2
US-08-147-812-4

```
Sequence 4, Application US/08147812
Patent No. 5766909
GENERAL INFORMATION:
APPLICANT: Xie, Qiao-wen
APPLICANT: Nathan, Carl F.
APPLICANT: Mumford, Richard A.
APPLICANT: Calaycay, Jimmy Ramos
TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh Centris650
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,812
FILING DATE: No. 5766909 Available
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/841,641
FILING DATE: 02-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 186581A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4041 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-147-812-4

Alignment Scores:
Pred. No.: 0.862 Length: 4041
Score: 60.00 Matches: 10
Percent Similarity: 72.22% Conservative: 3
Best Local Similarity: 55.56% Mismatches: 5
Query Match: 55.05% Indels: 0
Gaps: 0

US-09-371-347a-25 (1-18) x US-08-147-812-4 (1-4041)
Oy 1 G1yAlaMetTrPleupheGlyCysArgHisLysAspArgAspTyrLeuPhe 18
Db 3259 GGCCGATGAGCTTGTTGGTGGCGGACCCGAGGAGGACCACTCTAT 3312

RESULT 3
US-09-123-708-1
Sequence 1, Application US/09123708
Patent No. 6146887
GENERAL INFORMATION:
APPLICANT: SCHRADER, Jurgen
APPLICANT: GODECKE, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
FILE REFERENCE: 511169-2003
CURRENT APPLICATION NUMBER: US/09/123,708
EARLIER FILING DATE: 1998-07-28
EARLIER APPLICATION NUMBER: 08/553,503
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: P4411402.8
```

```
EARLIER FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4110
TYPE: DNA
ORGANISM: Cytomegalovirus
US-09-123-708-1

Alignment Scores:
Pred. No.: 0.88 Length: 4110
Score: 60.00 Matches: 10
Percent Similarity: 72.22% Conservative: 3
Best Local Similarity: 55.56% Mismatches: 5
Query Match: 55.05% Indels: 0
Gaps: 0

US-09-371-347a-25 (1-18) x US-09-123-708-1 (1-4110)
Oy 1 G1yAlaMetTrPleupheGlyCysArgHisLysAspArgAspTyrLeuPhe 18
Db 3195 GGCCGATGAGCTTGTTGGTGGCGGACCCGAGGAGGACCACTCTAT 3248

RESULT 4
US-09-123-624-1
Sequence 1, Application US/09123624
Patent No. 6149936
GENERAL INFORMATION:
APPLICANT: SCHRADER, Jurgen
APPLICANT: GODECKE, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
FILE REFERENCE: 511169-2004
CURRENT APPLICATION NUMBER: US/09/123,624
CURRENT FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 08/553,503
PRIOR FILING DATE: 1996-03-01
PRIOR APPLICATION NUMBER: 4411402.8
PRIOR FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4110
TYPE: DNA
ORGANISM: Mus musculus
US-09-123-624-1

Alignment Scores:
Pred. No.: 0.88 Length: 4110
Score: 60.00 Matches: 10
Percent Similarity: 72.22% Conservative: 3
Best Local Similarity: 55.56% Mismatches: 5
Query Match: 55.05% Indels: 0
Gaps: 0

US-09-371-347a-25 (1-18) x US-09-123-624-1 (1-4110)
Oy 1 G1yAlaMetTrPleupheGlyCysArgHisLysAspArgAspTyrLeuPhe 18
Db 3195 GGCCGATGAGCTTGTTGGTGGCGGACCCGAGGAGGACCACTCTAT 3248

RESULT 5
US-08-147-812-6
Sequence 6, Application US/08147812
Patent No. 5766909
GENERAL INFORMATION:
APPLICANT: Xie, Qiao-wen
APPLICANT: Nathan, Carl F.
APPLICANT: Mumford, Richard A.
APPLICANT: Calaycay, Jimmy Ramos
TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
```


ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh Centris650
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147, 812
FILING DATE: No. 5766909 Available
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/841, 641
FILING DATE: 02-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mallen, John W III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 186581A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-147-812-6
Alignment Scores:
Pred. No.: 0.894 Length: 4165
Score: 60.00 Matches: 10
Percent Similarity: 72.22% Conservative: 3
Best Local Similarity: 55.56% Mismatches: 5
Query Match: 55.05% Indels: 0
DB: 1 Gaps: 0
US-09-371-347a-25 (1-18) x US-08-147-812-6 (1-4165)
Qy 1 GlyAlaMetTrpLeuPheGlyCysArgHisLysAspArgAspTyrLeuPhe 18
Db 3259 GGCCGATGACCTTGCTGTGGTGCCGCGAGGAGGAGACCTCTAT 3312
RESULT 6
US-08-553-279-1
Sequence 1, Application US/08553279
Patent No. 5801024
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: No. 5801024el oxidoreductase from filamentous funghi,
TITLE OF INVENTION: DNA coding therefore and cells transformed with said DNA.
NUMBER OF SEQUENCES: 9
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553, 279
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP PCT/NL94/00135
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3701 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-553-279-1
Alignment Scores:
Pred. No.: 1.73 Length: 3701
Score: 58.00 Matches: 10
Percent Similarity: 66.67% Conservative: 2
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 53.21% Indels: 0
DB: 1 Gaps: 0
US-09-371-347a-25 (1-18) x US-08-553-279-1 (1-3701)
Qy 1 GlyAlaMetTrpLeuPheGlyCysArgHisLysAspArgAspTyrLeuPhe 18
Db 2298 GGACCACTGTCCTCTCTCGTTGCCGCAAGATGACGAGATTCTGTAC 2351
RESULT 7
US-09-126-109-11
Sequence 11, Application US/09126109
Patent No. 6171856
GENERAL INFORMATION:
APPLICANT: Thigpen, Anice
APPLICANT: Hohmeier, Hans-Ewald
APPLICANT: Newgard, Christopher B.
APPLICANT: Unger, Roger H.
APPLICANT: Shimabukuro, Michio
APPLICANT: Chen, Guaxun
APPLICANT: Rhodes, Christopher J.
APPLICANT: Hugl, Sigrun R.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126, 109
FILING DATE: 30-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055, 092
FILING DATE: 30-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US Unknown
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSJSD:560
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

CLONE. PHNOS
POSITION IN GENOME:

ORIGINAL SOURCE:

ORIGINAL SOURCE:

```

; TISSUE TYPE: Induced Human Hepatocyte RNA
; IMMEDIATE SOURCE:
; LIBRARY: Lambda Zap II CDNA
; CLONE: PHINOS
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..3668
; IDENTIFICATION METHOD: Experiment
; US-08-265-046-1

Alignment Scores:
Pred. No.: 6.65 Length: 4145
Score: 55.00 Matches: 9
Percent Similarity: 66.67% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 50.46% Indels: 0
DB: 1 Gaps: 0

US-09-371-347A-25 (1-18) x US-08-265-046-1 (1-4145)

Oy 1 GtAAlaMeTrPLeuPhHeGlyCysArGHisLysAspArgAspTyrLeuPhe 18
Db 3228 GGGCCGATGACCTTGTTGGTGGTCCGCCGCCGACAGATGAGACCATCTAC 3281

RESULT 10
; Sequence 1, Application US/08465522
; Patent No. 5882908
; GENERAL INFORMATION:
; APPLICANT: Billiar, Timothy R.
; APPLICANT: Nussler, Andreas K.
; APPLICANT: Geller, David A.
; APPLICANT: Simmons, Richard L.
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric
; TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market St. Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,522
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 116972-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
```

```

; DESCRIPTION: Synthase cDNA Clone
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Induced Human Hepatocyte RNA
; IMMEDIATE SOURCE:
; LIBRARY: Lambda Zap II CDNA
; CLONE: PHINOS
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..3668
; IDENTIFICATION METHOD: Experiment
; US-08-465-522-1

Alignment Scores:
Pred. No.: 6.65 Length: 4145
Score: 55.00 Matches: 9
Percent Similarity: 66.67% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 50.46% Indels: 0
DB: 2 Gaps: 0

US-09-371-347A-25 (1-18) x US-08-465-522-1 (1-4145)

Oy 1 GtAAlaMeTrPLeuPhHeGlyCysArGHisLysAspArgAspTyrLeuPhe 18
Db 3228 GGGCCGATGACCTTGTTGGTGGTCCGCCGCCGACAGATGAGACCATCTAC 3281

RESULT 11
; Sequence 1, Application PCTUS9311401
; GENERAL INFORMATION:
; APPLICANT: Billiar, Timothy R.
; APPLICANT: Nussler, Andreas K.
; APPLICANT: Geller, David A.
; APPLICANT: Simmons, Richard L.
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric
; TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold B. Silverman
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 600 Grant Street, 42nd Floor
; CITY: Pittsburgh
; STATE: PA
; COUNTRY: USA
; ZIP: 15219
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11401
; FILING DATE: 25-NOV-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/981,344
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Arnold B.
; REGISTRATION NUMBER: 22,614
; REFERENCE/DOCKET NUMBER: 116972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (412) 566-6000
; TELEFAX: (412) 566-6099
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 4145 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE: Induced Human Hepatocyte RNA
IMMEDIATE SOURCE:
LIBRARY: Lambda Zap II CDNA
CLONE: PHINOS
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: CDS
LOCATION: 207..3668
IDENTIFICATION METHOD: Experiment
PCT-US93-11401-1

Alignment Scores:
Pred. No.: 6.65 Length: 4145
Score: 55.00 Matches: 9
Percent Similarity: 66.67% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 50.46% Indels: 0
DB: 5 Gaps: 0

US-09-371-347A-25 (1-18) x PCT-US93-11401-1 (1-4145)

Qy 1 GYAlaMeTtRleuPhHeGlyCysArGHisLysAspArgAspTyrLeuPhe 18
Db 3228 GCCCGCATGACCTTGTTGGTGGCGCCGCCGACATGAGACACATCTAC 3281

RESULT 12

PCT-US95-07849-1

; Sequence 1, Application PC/TUS9507849

; GENERAL INFORMATION:

; APPLICANT: University of Pittsburgh of the Commonwealth System of Higher

; APPLICANT: Education

; TITLE OF INVENTION: Inducible Nitric Oxide Synthase

; TITLE OF INVENTION: Gene for Treatment of Disease

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lewis F. Gould, Jr.

; STREET: 1700 Market Street, Suite 3232

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/07849

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Gould, Lewis F. Jr.

; REGISTRATION NUMBER: 25,057

; REFERENCE/DOCKET NUMBER: 119130-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 575-6020

; TELEFAX: (215) 575-6015

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4145 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
SYNTHASE cDNA Clone
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE: Induced Human Hepatocyte RNA
IMMEDIATE SOURCE:
LIBRARY: Lambda Zap II CDNA
CLONE: PHINOS
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: CDS
LOCATION: 207..3668
IDENTIFICATION METHOD: Experiment
PCT-US95-07849-1

Alignment Scores:
Pred. No.: 6.65 Length: 4145
Score: 55.00 Matches: 9
Percent Similarity: 66.67% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 50.46% Indels: 0
DB: 5 Gaps: 0

US-09-371-347A-25 (1-18) x PCT-US95-07849-1 (1-4145)

Qy 1 GYAlaMeTtRleuPhHeGlyCysArGHisLysAspArgAspTyrLeuPhe 18
Db 3228 GCCCGCATGACCTTGTTGGTGGCGCCGCCGACATGAGACACATCTAC 3281

RESULT 13

US-09-134-001C-1557

; Sequence 1557, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 1557

; LENGTH: 1890

; TYPE: DNA

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-1557

Alignment Scores:
Pred. No.: 5.75 Length: 1890
Score: 53.00 Matches: 9
Percent Similarity: 66.67% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 48.62% Indels: 0
DB: 4 Gaps: 0

US-09-371-347A-25 (1-18) x US-09-134-001C-1557 (1-1890)

Qy 1 GYAlaMeTtRleuPhHeGlyCysArGHisLysAspArgAspTyrLeuPhe 18
Db 1531 GGAATACATGCTTATCTTTGGAGATCAACACTTCACTACAGATTTCTGTAT 1584

RESULT 14
US-09-302-620B-82
: Sequence 82, Application US/09302620B
: Patent No. 6331420
: GENERAL INFORMATION:
: APPLICANT: Wilson, C. Ron
: APPLICANT: Craft, David L.
: APPLICANT: Eitich, Dudley
: APPLICANT: Eshoo, Mark
: APPLICANT: Madduri, Krishna M.
: APPLICANT: Cornett, Cathy A.
: APPLICANT: Brenner, Alfred A.
: APPLICANT: Tang, Maria
: APPLICANT: Loper, John C.
: APPLICANT: Gleson, Martin
: TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
: TITLE OF INVENTION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
: TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
: FILE REFERENCE: 1010-16.seq
: CURRENT APPLICATION NUMBER: US/09/302,620B
: CURRENT FILING DATE: 1999-04-30
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 82
: LENGTH: 4145
: TYPE: DNA
: ORGANISM: Candida tropicalis
US-09-302-620B-82

Alignment Scores:
Pred. No.: 14.9 Length: 4145
Score: 53.00 Matches: 8
Percent Similarity: 72.22% Conservative: 5
Best Local Similarity: 44.44% Mismatches: 5
Query Match: 48.62% Indels: 0
DB: 4 Gaps: 0

US-09-371-347A-25 (1-18) x US-09-302-620B-82 (1-4145)

Qy 1 G1yAlametrPleuphepGlyCysArghIsLysAspArgAspTyrLeuphe 18
Db 2707 GGCAAGACTTGTGTTTATGTTGCGAAGAACTCCACGAGACTTTTGTAC 2760

RESULT 15

US-09-302-620B-81
: Sequence 81, Application US/09302620B
: Patent No. 6331420
: GENERAL INFORMATION:
: APPLICANT: Wilson, C. Ron
: APPLICANT: Craft, David L.
: APPLICANT: Eitich, Dudley
: APPLICANT: Eshoo, Mark
: APPLICANT: Madduri, Krishna M.
: APPLICANT: Cornett, Cathy A.
: APPLICANT: Brenner, Alfred A.
: APPLICANT: Tang, Maria
: APPLICANT: Loper, John C.
: APPLICANT: Gleson, Martin
: TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
: TITLE OF INVENTION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
: TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
: FILE REFERENCE: 1010-16.seq
: CURRENT APPLICATION NUMBER: US/09/302,620B
: CURRENT FILING DATE: 1999-04-30
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 81
: LENGTH: 4206
: TYPE: DNA
: ORGANISM: Candida tropicalis
US-09-302-620B-81

Alignment Scores:
Pred. No.: 15.1 Length: 4206
Score: 53.00 Matches: 8
Percent Similarity: 72.22% Conservative: 5
Best Local Similarity: 44.44% Mismatches: 5
Query Match: 48.62% Indels: 0
DB: 4 Gaps: 0

US-09-371-347A-25 (1-18) x US-09-302-620B-81 (1-4206)

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Db 2680 GGCAAGACTTGTGTTTATGTTGCGAAGAACTCCACGAGACTTTTGTAC 2733

Search completed: July 29, 2003, 23:04:05
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 29, 2003, 10:56:19 ; Search time 425.084 Seconds
(without alignments)
10177.082 Million cell updates/sec

Title: US-09-371-347A-41

Perfect score: 2097
Sequence: 1 atgagagaggttcgtctact.....ttcagatattgttcataa 2097

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2097	100.0	2097	12	US-09-371-347-41 Sequence 41, Appl
2	2095.4	99.9	2097	12	US-09-371-347-1 Sequence 1, Appl
3	2095.4	99.9	3259	12	US-09-371-347-24 Sequence 24, Appl
4	2093.8	99.8	2097	12	US-09-371-347-43 Sequence 43, Appl
5	2079.4	99.2	2094	12	US-09-371-347-45 Sequence 45, Appl
6	2077.4	99.1	2093	12	US-09-371-347-47 Sequence 47, Appl
7	174.4	8.3	2475	12	US-09-909-567B-38 Sequence 38, Appl
8	88.6	4.2	1872	11	US-09-917-800A-1351 Sequence 1351, Ap
9	88.6	4.2	2401	11	US-09-917-800A-1397 Sequence 1397, Ap
10	83.8	4.0	101	11	US-09-783-590-1364 Sequence 1364, Ap
11	61	2.9	298	10	US-09-294-093B-4842 Sequence 4842, Ap
12	59.6	2.8	2470	10	US-09-822-849A-278 Sequence 278, App
13	58.4	2.8	230	10	US-09-923-876-2845 Sequence 2845, Ap
14	57.2	2.7	13508	8	US-08-781-986A-120 Sequence 120, App
15	56	2.7	2136	11	US-09-938-842A-803 Sequence 803, App
16	54.8	2.6	2403	11	US-09-880-107-3039 Sequence 3039, Ap

17	53.6	2.6	1863	10	US-09-765-873A-13 Sequence 13, Appl
18	52.2	2.5	411	10	US-09-925-299-440 Sequence 440, App
19	52.2	2.5	411	12	US-09-925-299-440 Sequence 440, App
20	50.6	2.4	2088	15	US-10-128-714-7234 Sequence 7234, Ap
21	50.2	2.4	1448	10	US-09-939-980-113 Sequence 113, App
22	49.2	2.3	1944	15	US-10-272-017A-4 Sequence 4, Appl
23	49.2	2.3	3037	10	US-09-911-781-3 Sequence 3, Appl
24	49.2	2.3	4145	10	US-09-911-781-3 Sequence 3, Appl
25	49.2	2.3	4145	12	US-09-976-800-82 Sequence 82, Appl
26	49.2	2.3	4145	15	US-10-138-838-82 Sequence 82, Appl
27	49.2	2.3	4145	15	US-10-139-031-82 Sequence 82, Appl
28	49.2	2.3	4145	15	US-10-138-905-82 Sequence 82, Appl
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33	46.4	2.2	1845	15	US-10-128-714-2234 Sequence 2234, Ap
34	46.4	2.2	2145	15	US-10-128-714-5234 Sequence 5234, Ap
35	46.4	2.2	3845	15	US-10-128-714-234 Sequence 234, App
36	46.4	2.2	4145	15	US-10-128-714-5234 Sequence 5234, Ap
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38	46	2.2	4206	10	US-09-911-781-2 Sequence 2, Appl
39	46	2.2	4206	12	US-09-976-800-81 Sequence 81, Appl
40	46	2.2	4206	15	US-10-138-838-81 Sequence 81, Appl
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43	46	2.2	4206	15	US-10-138-916-81 Sequence 81, Appl
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ALIGNMENTS

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RESULT 1
US-09-371-347-41
: Sequence 41, Application US/09371347
: Publication No. US20030082676A1
: GENERAL INFORMATION:
: APPLICANT: Roy A. Gravel et al.
: TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
: TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
: TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
: FILE REFERENCE: 50004/003003
: CURRENT APPLICATION NUMBER: US/09/371,347
: CURRENT FILING DATE: 1999-08-10
: PRIOR APPLICATION NUMBER: 60/071,622
: PRIOR FILING DATE: 1998-01-16
: PRIOR APPLICATION NUMBER: 09/232,028
: PRIOR FILING DATE: 1999-01-15
: NUMBER OF SEQ ID NOS: 51
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 41
: LENGTH: 2097
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-371-347-41

Query Match      100.0%; Score 2097; DB 12; Length 2097;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 ATGAGAGGTTCTGTTACTATATGCTACACGACGAGGCAAGGCCATCCAGAA 60
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OY      61 GAAATATGAGACCAAGCTGTGATCATGATTTTCGAGATCTTCACTGTATTTAGTGA 120
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DB      61 GAAATATGAGACCAAGCTGTGATCATGATTTTCGAGATCTTCACTGTATTTAGTGA 120
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OY      121 TCCGATAGATATGACCTAAACCAAGACGCTCTTGTGTGTGTGTTCTACACAG 180
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361 CGGCAATTTCTATGACACTGACATGACATGACTGTGAGTTTGAAGCTTGTGTTAG 420
361 CGGCAATTTCTATGACACTGACATGACATGACTGTGAGTTTGAAGCTTGTGTTAG 420
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481 GAGAGATTAAGTGGGCACTCCCGGTGGCATCACCCTGATCCTTGAGGACAGACCTTGTG 540
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1681 AATCTCAG 1740
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US-09-371-347-1
; Sequence 1, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHYLONLINE SYNTHASE REDUCTASE;
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 51
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 ; SEQ ID NO 1
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 ; ORGANISM: Homo sapiens
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 DB 361 CGGCACTTCTATGACACTGACATGAGATGAGTGTAGAGTTTAAACCTTGGTTGAG 420
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 DB 421 CCGTGATTTGCTGGAGCTGCGCCAGCCCTCAGAAACATTTTAAAGTCAAGCAAGACAA 480
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 DB 481 GAGGAGATATAGTGGCCACTCCCGGTGGCATCTGACATCTTGAAGGACAGACTTGG 540
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 QY 1741 AGGCATATAGATAGGATTTATCTATTCAGAAAAAGACTCGAATTTCTTAAGCATGGG 1800
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 QY 1801 ATCTTAATCTATTAAGGTTTCTCTTCTCAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
 DB 1801 ATCTTAATCTATTAAGGTTTCTCTTCTCAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
 QY 1861 CCAGCAAGATATGATACAGCAACATCCAGCTTCAAGGAGGAGGAGGAGAAATCTC 1920
 DB 1861 CCAGCAAGATATGATACAGCAACATCCAGCTTCAAGGAGGAGGAGGAGAAATCTC 1920
 QY 1921 CTCACAGAGAAAGCCATATTTATGTGTGAGAGATGCAAGAATATGCGCAAGATGTA 1980
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 QY 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGTTAAAAAATCTAGAACATG 2040

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RESULT 3

US-09-371-347-24
; Sequence 24, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371.347
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 3259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-24

Query Match 99.9%; Score 2095.4; DB 12; Length 3259;

Best Local Similarity 100.0%; Pred No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAGGTTTCTGTACTATATGCTACACAGCAGGAGAGGCAAGCCATCGAGAA 60
Db ATGAGAGGTTTCTGTACTATATGCTACACAGCAGGAGAGGCAAGCCATCGAGAA 139
QY 61 GAAATGTGAGAACCTGTGACATGATTTTCTGCAATCTTACTGATTAAGTAA 120
Db GAAATGTGAGAACCTGTGACATGATTTTCTGCAATCTTACTGATTAAGTAA 199
QY 121 TCCGATATGATGACATAAAACCCGAAGAGCTCCTTGTGTTGTTCTTACCAAG 180
Db TCCGATATGATGACATAAAACCCGAAGAGCTCCTTGTGTTGTTCTTACCAAG 259
QY 200 TCCGATATGATGACATAAAACCCGAAGAGCTCCTTGTGTTGTTCTTACCAAG 259
Db TCCGATATGATGACATAAAACCCGAAGAGCTCCTTGTGTTGTTCTTACCAAG 319
QY 181 GGCACCGGAGACCCACCGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
Db GGCACCGGAGACCCACCGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 319
QY 241 CTGGCGGTGATTTCTTCTGCTACCTGCGGTATGGTTACTGGTCTGGTATTCAGAA 300
Db CTGGCGGTGATTTCTTCTGCTACCTGCGGTATGGTTACTGGTCTGGTATTCAGAA 379
QY 320 CTGGCGGTGATTTCTTCTGCTACCTGCGGTATGGTTACTGGTCTGGTATTCAGAA 379
Db CTGGCGGTGATTTCTTCTGCTACCTGCGGTATGGTTACTGGTCTGGTATTCAGAA 439
QY 301 TACACCTACTTTTGAATGGGGAGAGATTTGATTAACGACTTCANAGCTTGGAGCC 360
Db TACACCTACTTTTGAATGGGGAGAGATTTGATTAACGACTTCANAGCTTGGAGCC 439
QY 380 TACACCTACTTTTGAATGGGGAGAGATTTGATTAACGACTTCANAGCTTGGAGCC 439
Db TACACCTACTTTTGAATGGGGAGAGATTTGATTAACGACTTCANAGCTTGGAGCC 499
QY 361 CGGCAATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATG 420
Db CGGCAATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATG 499
QY 440 CGGCAATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATG 499
Db CGGCAATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATG 559
QY 421 CCGTGATTTGCTGAGACTGCGGACACCTCAGAAAGCATTTTASGTCAAGCAGAGACAA 480
Db CCGTGATTTGCTGAGACTGCGGACACCTCAGAAAGCATTTTASGTCAAGCAGAGACAA 559
QY 500 CCGTGATTTGCTGAGACTGCGGACACCTCAGAAAGCATTTTASGTCAAGCAGAGACAA 559
Db CCGTGATTTGCTGAGACTGCGGACACCTCAGAAAGCATTTTASGTCAAGCAGAGACAA 599
QY 481 GAGAGATTAAGTGGGAGACTCCCGGTGGACATCCTGATCCTTAGAGACAGACTTGG 540
Db GAGAGATTAAGTGGGAGACTCCCGGTGGACATCCTGATCCTTAGAGACAGACTTGG 619
QY 560 GAGAGATTAAGTGGGAGACTCCCGGTGGACATCCTGATCCTTAGAGACAGACTTGG 619
Db GAGAGATTAAGTGGGAGACTCCCGGTGGACATCCTGATCCTTAGAGACAGACTTGG 699
QY 541 AAGTCAGAGCTGTACATTAATCTCAAGTCGAGCTTGTGAGATTTGATGATTCAGAA 600
Db AAGTCAGAGCTGTACATTAATCTCAAGTCGAGCTTGTGAGATTTGATGATTCAGAA 600

Db 620 AAGTCAGAGCTGTACATTAATCTCAAGTCGAGCTTGTGAGATTTGATGATTCAGAA 679
QY 601 AGAAGGATTTCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCATATGTTGA 660
Db AGAAGGATTTCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCATATGTTGA 739
QY 680 AGAAGGATTTCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCATATGTTGA 739
Db AGAAGGATTTCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCATATGTTGA 799
QY 661 ATTGAAGCTTTGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 720
Db ATTGAAGCTTTGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 799
QY 740 ATTGAAGCTTTGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 799
Db ATTGAAGCTTTGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 859
QY 721 AATATTCCTGCTTACCCCGACCAATATTTACAGTATCTGACAGAGTCTGTTGGCAG 780
Db AATATTCCTGCTTACCCCGACCAATATTTACAGTATCTGACAGAGTCTGTTGGCAG 859
QY 800 AATATTCCTGCTTACCCCGACCAATATTTACAGTATCTGACAGAGTCTGTTGGCAG 859
Db AATATTCCTGCTTACCCCGACCAATATTTACAGTATCTGACAGAGTCTGTTGGCAG 880
QY 781 GAGGAAAGCAAGTATCTGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 840
Db GAGGAAAGCAAGTATCTGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 919
QY 860 GAGGAAAGCAAGTATCTGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 919
Db GAGGAAAGCAAGTATCTGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 979
QY 841 GCAGTTCAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 900
Db GCAGTTCAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 979
QY 920 GCAGTTCAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 979
Db GCAGTTCAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 1039
QY 901 TCAATATCAGACTTTCTGATGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 960
Db TCAATATCAGACTTTCTGATGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 1039
QY 980 TCAATATCAGACTTTCTGATGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 1039
Db TCAATATCAGACTTTCTGATGAGTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 1099
QY 961 GATTCTGAGTACCAAGCTCTACCAAGCTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 1020
Db GATTCTGAGTACCAAGCTCTACCAAGCTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 1099
QY 1040 GATTCTGAGTACCAAGCTCTACCAAGCTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 1099
Db GATTCTGAGTACCAAGCTCTACCAAGCTCTGACATTAACCGTGGGTACCCCGACCTCTCACAGCCCTGCTG 1159
QY 1021 GTCTTTTGAATTAAGGAGCAGACAGCAAGAAAGAGAGTACCTTACCCGACATTA 1080
Db GTCTTTTGAATTAAGGAGCAGACAGCAAGAAAGAGAGTACCTTACCCGACATTA 1159
QY 1100 GTCTTTTGAATTAAGGAGCAGACAGCAAGAAAGAGAGTACCTTACCCGACATTA 1159
Db GTCTTTTGAATTAAGGAGCAGACAGCAAGAAAGAGAGTACCTTACCCGACATTA 1219
QY 1141 AAAAAGCAATTTTGGGAGCCCTTGTGAGTATACAGTACAGTCTGAAAAGGAGCAGG 1200
Db AAAAAGCAATTTTGGGAGCCCTTGTGAGTATACAGTACAGTCTGAAAAGGAGCAGG 1279
QY 1220 AAAAAGCAATTTTGGGAGCCCTTGTGAGTATACAGTACAGTCTGAAAAGGAGCAGG 1279
Db AAAAAGCAATTTTGGGAGCCCTTGTGAGTATACAGTACAGTCTGAAAAGGAGCAGG 1339
QY 1201 CTACAGAGCTGTGACATTAACAGGAGGAGCCGATTAATAGCCGCTTTGTACGAGATGCC 1260
Db CTACAGAGCTGTGACATTAACAGGAGGAGCCGATTAATAGCCGCTTTGTACGAGATGCC 1339
QY 1280 CTACAGAGCTGTGACATTAACAGGAGGAGCCGATTAATAGCCGCTTTGTACGAGATGCC 1339
Db CTACAGAGCTGTGACATTAACAGGAGGAGCCGATTAATAGCCGCTTTGTACGAGATGCC 1399
QY 1261 TGTGCTGCTGTGATGATCTCCGCTGCTTCCCTTGTGAGCAGCAGCAGTCTGCTG 1320
Db TGTGCTGCTGTGATGATCTCCGCTGCTTCCCTTGTGAGCAGCAGCAGTCTGCTG 1399
QY 1340 TGTGCTGCTGTGATGATCTCCGCTGCTTCCCTTGTGAGCAGCAGCAGTCTGCTG 1399
Db TGTGCTGCTGTGATGATCTCCGCTGCTTCCCTTGTGAGCAGCAGCAGTCTGCTG 1459
QY 1321 CTGCTGCAACATCTTCTTAACCTCAACCCAGACCATATTTCTGTGCAAGCTCAAGTTTA 1380
Db CTGCTGCAACATCTTCTTAACCTCAACCCAGACCATATTTCTGTGCAAGCTCAAGTTTA 1459
QY 1400 CTGCTGCAACATCTTCTTAACCTCAACCCAGACCATATTTCTGTGCAAGCTCAAGTTTA 1459
Db CTGCTGCAACATCTTCTTAACCTCAACCCAGACCATATTTCTGTGCAAGCTCAAGTTTA 1519
QY 1381 TTTTCAACCAAGAAAGCTCATTGTTCTTCAACATTTGGAATTTCTGTCACTGCCACA 1440
Db TTTTCAACCAAGAAAGCTCATTGTTCTTCAACATTTGGAATTTCTGTCACTGCCACA 1519
QY 1460 TTTTCAACCAAGAAAGCTCATTGTTCTTCAACATTTGGAATTTCTGTCACTGCCACA 1519
Db TTTTCAACCAAGAAAGCTCATTGTTCTTCAACATTTGGAATTTCTGTCACTGCCACA 1579
QY 1441 ACAGAGGTTCTGCGGAAGGAGATGATGACAGGCTGGCTGCTTGTGTTGCTTCACTG 1500
Db ACAGAGGTTCTGCGGAAGGAGATGATGACAGGCTGGCTGCTTGTGTTGCTTCACTG 1579
QY 1501 CTTTCAAGCAACATCTCATGATCCCATGAAGACAGCGGAAAGCCCTGGCTCTTAAGATA 1560
Db CTTTCAAGCAACATCTCATGATCCCATGAAGACAGCGGAAAGCCCTGGCTCTTAAGATA 1639
QY 1580 CTTTCAAGCAACATCTCATGATCCCATGAAGACAGCGGAAAGCCCTGGCTCTTAAGATA 1639
Db CTTTCAAGCAACATCTCATGATCCCATGAAGACAGCGGAAAGCCCTGGCTCTTAAGATA 1699
QY 1561 TCCATCTCTCTGCAACAACAATTTCTTCACTTACAGATGACAGCCCTCAATCCCATC 1620
Db TCCATCTCTCTGCAACAACAATTTCTTCACTTACAGATGACAGCCCTCAATCCCATC 1699
QY 1640 TCCATCTCTCTGCAACAACAATTTCTTCACTTACAGATGACAGCCCTCAATCCCATC 1699
Db TCCATCTCTCTGCAACAACAATTTCTTCACTTACAGATGACAGCCCTCAATCCCATC 1759
QY 1621 AATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680
Db AATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1759

QY	1681	AAACTCCAAGAACAAACCCAGATGGAATTTTGGACCAATGTGCTTTTGGCTGC	1740
Db	1760	AAACTCCAAGAACAAACCCAGATGGAATTTTGGACCAATGTGCTTTTGGCTGC	1819
QY	1741	AGGCATTAAGTATAGGATTTATCTATTGAGAAAAGGTCAGACATTTTCCTTAACATGGG	1800
Db	1820	AGGCATTAAGTATAGGATTTATCTATTGAGAAAAGGTCAGACATTTTCCTTAACATGGG	1879
QY	1801	ATCTTAACTCATCTAAAGGTTTCCCTTCTCAAGAGATGCTCCTGTGTGGGAGAGAAAGCC	1860
Db	1880	ATCTTAACTCATCTAAAGGTTTCCCTTCTCAAGAGATGCTCCTGTGTGGGAGAGAAAGCC	1939
QY	1861	CCAGCAAAAGTATGTACAAAGACACATCCAGCTTCATGSCCAGCAGGTGGCAGATCTCTC	1920
Db	1940	CCAGCAAAAGTATGTACAAAGACACATCCAGCTTCATGSCCAGCAGGTGGCAGATCTCTC	1999
QY	1921	CTCCAGAGAAAGGGCCATATTTATGTGTGTGAGATGCCAAAGATATATGGCCAAAGATGTA	1980
Db	2000	CTCCAGAGAAAGGGCCATATTTATGTGTGTGAGATGCCAAAGATATATGGCCAAAGATGTA	2059
QY	1981	CATGATGCCCTTGTGCAAAATTAATTAAGCAAAAGAGTTTGAGTTTGA AAAACTGAAGCATG	2040
Db	2060	CATGATGCCCTTGTGCAAAATTAATTAAGCAAAAGAGTTTGAGTTTGA AAAACTGAAGCATG	2119
QY	2041	AAAAACCTGGCCACTTTAAAAAGAAAAAACGCTACTCTCAGGATATTTGGTCAATA	2097
Db	2120	AAAAACCTGGCCACTTTAAAAAGAAAAAACGCTACTCTCAGGATATTTGGTCAATA	2176

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RESULT 4
US-09-371-347-43
: Sequence 43, Application US/09371347
: Publication No. US20030082676A1
: GENERAL INFORMATION:
: APPLICANT: Roy A. Gravel et al.
: TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
: TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF
: TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
: FILE REFERENCE: 50004/003003
: CURRENT APPLICATION NUMBER: US/09/371,347
: CURRENT FILING DATE: 1999-08-10
: PRIOR APPLICATION NUMBER: 60/071,622
: PRIOR FILING DATE: 1998-01-16
: PRIOR APPLICATION NUMBER: 09/232,028
: PRIOR FILING DATE: 1999-01-15
: NUMBER OF SEQ ID NOS: 51
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 43
: LENGTH: 2097
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-371-347-43

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Query Match	99.8%;	Score 2093.8;	DB 12;	Length 2097;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 2095; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	ATGAGGAGGTTTCTGTTACTATATGCTACACAGCAGGACGCGCAAAAGCCATTCGACAGA	60
Db	1	ATGAGGAGGTTTCTGTTACTATATGCTACACAGCAGGACGCGCAAAAGCCATTCGACAGA	60
QY	61	GAAATATGTGAGCAGAGCTGTGTCATGAGATTTTCTGCAGATCTTCACGTATATAGGAA	120
Db	61	GAAATATGTGAGCAGAGCTGTGTCATGAGATTTTCTGCAGATCTTCACGTATATATGGA	120
QY	121	TCCGATAGTATGACCTTAAAAAACCGAAACAGCTCCTTGTGTTGTGTGTTCTACACAG	180
Db	121	TCCGATAGTATGACCTTAAAAAACCGAAACAGCTCCTTGTGTTGTGTGTTCTACACAG	180
QY	181	GGCACCGGAGACCCACCCGACACAGCCCGCAGAATTGTTAAAGAAATACAGAACCAACA	240
Db	181	GGCACCGGAGACCCACCCGACACAGCCCGCAGAATTGTTAAAGAAATACAGAACCAACA	240

Oy	241	CTGCCGGTGAATTTCTTTTGGCTCACCTCGCGGTATGGGTACTAGGGTCTCGGGTGAATTCAGAA	300
Db	241	CTGCCGGTGAATTTCTTTTGGCTCACCTCGCGGTATGGGTACTAGGGTCTCGGGTGAATTCAGAA	300
Oy	301	TACACCTACTTTTTCGAATGGGGGGGAAGATTAATTGATTAAGACATTCYCAAGAGCTTGAGACC	360
Db	301	TACACCTACTTTTTCGAATGGGGGGGAAGATTAATTGATTAAGACATTCYCAAGAGCTTGAGACC	360
Oy	361	CGGCAATTTCTATGACACCTGGACATGCAGATGACTGTGTAGGTTTGAACCTTTGTGGTTGAG	420
Db	361	CGGCAATTTCTATGACACCTGGACATGCAGATGACTGTGTAGGTTTGAACCTTTGTGGTTGAG	420
Oy	421	CCGTTGGAATGCTGGAGACTCTGGCCAGGCCCTCAGAAAGATTTTATAGTCACAGCAGAGCAAA	480
Db	421	CCGTTGGAATGCTGGAGACTCTGGCCAGGCCCTCAGAAAGATTTTATAGTCACAGCAGAGCAAA	480
Oy	481	GAGAGAGATTAAGTGGCGGCACTCCCGGTGGCATCACCTGCATCTTGTAGAGACAGACTTGTG	540
Db	481	GAGAGAGATTAAGTGGCGGCACTCCCGGTGGCATCACCTGCATCTTGTAGAGACAGACTTGTG	540
Oy	541	AAGTCAGAGCTGCTACACATTTGAATCTCAAGTCAGCTTCTGAGATTTCGATGATTCAGGA	600
Db	541	AAGTCAGAGCTGCTACACATTTGAATCTCAAGTCAGCTTCTGAGATTTCGATGATTCAGGA	600
Oy	601	AGAAAGGATTTCTGAGGTTTGAACCAAAATCAGATGAAACAGCAACCAATCAATGTTGTA	660
Db	601	AGAAAGGATTTCTGAGGTTTGAACCAAAATCAGATGAAACAGCAACCAATCAATGTTGTA	660
Oy	661	ATTGAGACATTTGAGTCCCTCACCTTACCCGTTGCGTACCCCCACCTCAGCAAGCCCTCTG	720
Db	661	ATTGAGACATTTGAGTCCCTCACCTTACCCGTTGCGTACCCCCACCTCAGCAAGCCCTCTG	720
Oy	721	AATATTCCTGGTTTACCCCGGAAATATTTACAGTACATGCGAGGAGTCTCTTGAGCAG	780
Db	721	AATATTCCTGGTTTACCCCGGAAATATTTACAGTACATGCGAGGAGTCTCTTGAGCAG	780
Oy	781	GAGGAAAGCCCAAGTATCTGTGACTTCAGCAGATCCAGTTTTCYCAAGTCCCAATTTTCAAG	840
Db	781	GAGGAAAGCCCAAGTATCTGTGACTTCAGCAGATCCAGTTTTCYCAAGTCCCAATTTTCAAG	840
Oy	841	GCACTTCACTTACTACGAATGATGCCATTAATAAACCACTCTGCTGTGTGAATTTGGACATT	900
Db	841	GCACTTCACTTACTACGAATGATGCCATTAATAAACCACTCTGCTGTGTGAATTTGGACATT	900
Oy	901	TCAATATACAGACTTTTCCCTATCAGCCCTGGAGATGCTTCACGCTGATCTGCGCTAACACT	960
Db	901	TCAATATACAGACTTTTCCCTATCAGCCCTGGAGATGCTTCACGCTGATCTGCGCTAACACT	960
Oy	961	GATTCTGAGTACAAAGCTACTCTCCAAAGACTCAGCTTGAAAGTAAAGAAGACACTGCG	1020
Db	961	GATTCTGAGTACAAAGCTACTCTCCAAAGACTCAGCTTGAAAGTAAAGAAGACACTGCG	1020
Oy	1021	GTCCTTTTGAATAAAGGCGAGACAAAGAAAGAAAGAGCTACTTACCACACATATA	1080
Db	1021	GTCCTTTTGAATAAAGGCGAGACAAAGAAAGAAAGAGCTACTTACCACACATATA	1080
Oy	1081	CCTCGGGGATGTTCTCTCCAGTATATTTTACCTGGTGTCTTGAATTCGAGCAATTTCT	1140
Db	1081	CCTCGGGGATGTTCTCTCCAGTATATTTTACCTGGTGTCTTGAATTCGAGCAATTTCT	1140
Oy	1141	AAAAAGCATTTTGGCAGCCCTGTGGACTATACCAAGTGCAGATGCTGTAAAGCGCAGG	1200
Db	1141	AAAAAGCATTTTGGCAGCCCTGTGGACTATACCAAGTGCAGATGCTGTAAAGCGCAGG	1200
Oy	1201	CTACAGAGAGCTGTGACATTAACAAGGGGAGCCCATTAATAGCCCTTTGTACAGATAGCC	1260
Db	1201	CTACAGAGAGCTGTGACATTAACAAGGGGAGCCCATTAATAGCCCTTTGTACAGATAGCC	1260
Oy	1261	TGTGCTGCTGTTGTTGGATCTCTCTCTCTGCTTCCCTTCTTGCAGCCACCACTAGTCTC	1320
Db	1261	TGTGCTGCTGTTGTTGGATCTCTCTCTCTCTGCTTCCCTTCTTGCAGCCACCACTAGTCTC	1320

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OY 1321 CTGCTCGAACAATCTTCTAACTGACACCAACCATATTCGTGACAGTCAAGTTA 1380
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DB 1321 CTGCTCGAACAATCTTCTAACTGACACCAACCATATTCGTGACAGTCAAGTTA 1380
OY 1381 TTTCAACCCAGGAAGACTGCTATTTTGTCTTCAACATTTGGAGATTTTCTGTCTACGCCACA 1440
    |||||||
DB 1381 TTTCAACCCAGGAAGACTGCTATTTTGTCTTCAACATTTGGAGATTTTCTGTCTACGCCACA 1440
OY 1441 ACAGAGGTTCTCGGAAGGAGATGTACAGGCTGGGCGCTTGTGGTGTCTTCAGAT 1500
    |||||||
DB 1441 ACAGAGGTTCTCGGAAGGAGATGTACAGGCTGGGCGCTTGTGGTGTCTTCAGAT 1500
OY 1501 CTTCAGCCAAACATACATGATCCCATGAAGACAGCGGGAAGCCCTGGCTCTTAAGATA 1560
    |||||||
DB 1501 CTTCAGCCAAACATACATGATCCCATGAAGACAGCGGGAAGCCCTGGCTCTTAAGATA 1560
OY 1561 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCAATC 1620
    |||||||
DB 1561 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCAATC 1620
OY 1621 ATATGCTGGGTCCAGGAACCGCATAGCCCGCTTATTTGGGTCTCAACATAGAGAG 1680
    |||||||
DB 1621 ATATGCTGGGTCCAGGAACCGCATAGCCCGCTTATTTGGGTCTCAACATAGAGAG 1680
OY 1681 AAATCTCAAGAAACAACCCAGAGTGAATTTTGGAGCAATGTGTTTGTGCTGC 1740
    |||||||
DB 1681 AAATCTCAAGAAACAACCCAGAGTGAATTTTGGAGCAATGTGTTTGTGCTGC 1740
OY 1741 AGGCAATAGAGATAGGATTTATCTATTCAGAAAAGCTCAGACATTTCTTACGATGG 1800
    |||||||
DB 1741 AGGCAATAGAGATAGGATTTATCTATTCAGAAAAGCTCAGACATTTCTTACGATGG 1800
OY 1801 ATCTTAATCTATCTTAAAGTTTCTCTTCAAGAGATGCTCCGTGGTGGGAGAGGAGACC 1860
    |||||||
DB 1801 ATCTTAATCTATCTTAAAGTTTCTCTTCAAGAGATGCTCCGTGGTGGGAGAGGAGACC 1860
OY 1861 CCAGCAAAAGTATGTACAAGACAACATCCAGCTTCATGSCCAGAGGTGGCGAATCTCTC 1920
    |||||||
DB 1861 CCAGCAAAAGTATGTACAAGACAACATCCAGCTTCATGSCCAGAGGTGGCGAATCTCTC 1920
OY 1921 CTCCAGAGGAAGGCGCATTTATGTGTGAGAGTGAAGAAATATGGCCCAAGATGTA 1980
    |||||||
DB 1921 CTCCAGAGGAAGGCGCATTTATGTGTGAGAGTGAAGAAATATGGCCCAAGATGTA 1980
OY 1981 CATGATGCCCTTGTGCAATATATAAGCAAGAGGTGAGTTGAAAACTGAAAGCATG 2040
    |||||||
DB 1981 CATGATGCCCTTGTGCAATATATAAGCAAGAGGTGAGTTGAAAACTGAAAGCATG 2040
OY 2041 AAAACCCCTGGCCACTTTAAAGAGAAAACGCTACCTTCAGATATTTGTCATAA 2097
    |||||||
DB 2041 AAAACCCCTGGCCACTTTAAAGAGAAAACGCTACCTTCAGATATTTGTCATAA 2097

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RESULT 5

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: Sequence 45, Application US/09371347
: Publication No. US20030082676a1

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: GENERAL INFORMATION:

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: APPLICANT: Roy A. Gravel et al.

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```

: TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:

```

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: TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE

```

```

: FILE REFERENCE: 50004/003003

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: CURRENT APPLICATION NUMBER: US/09/371.347

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: PRIOR FILING DATE: 1999-08-10

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: PRIOR APPLICATION NUMBER: 60/071,622

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: PRIOR FILING DATE: 1998-01-16

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: PRIOR APPLICATION NUMBER: 09/232,028

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: NUMBER OF SEQ ID NOS: 51

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: SOFTWARE: FastSeq for Windows Version 4.0

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: SEQ ID NO 45

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: LENGTH: 2094

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: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-371-347-45

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Query Match          99.2%; Score 2079.4; DB 12; Length 2094;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

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OY 1 ATGAGAGAGTTTCTTCTATCTATATCTCTACACAGCAGGACAGGACCAAGCCATCGCAGAA 60
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DB 1 ATGAGAGAGTTTCTTCTATCTATATCTCTACACAGCAGGACAGGACCAAGCCATCGCAGAA 60
OY 61 GAAATATGTGAGCAAGCTGTGTATCATGATTTTGTGAGATCTTCACTGATATTGAGTAA 120
    |||||||
DB 61 GAAATATGTGAGCAAGCTGTGTATCATGATTTTGTGAGATCTTCACTGATATTGAGTAA 120
OY 121 TCCGATTAAGTATGACCTTAAACCCGAAACAGCTCTCTGTTGTTGTTGTTTCAACACG 180
    |||||||
DB 121 TCCGATTAAGTATGACCTTAAACCCGAAACAGCTCTCTGTTGTTGTTGTTTCAACACG 180
OY 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGACCAACA 240
    |||||||
DB 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGACCAACA 240
OY 241 CTGCCGGTTGATTTCTTGTCTACCTGCGGTATGGGTACTGCGTCTGCGTATTCAGAA 300
    |||||||
DB 241 CTGCCGGTTGATTTCTTGTCTACCTGCGGTATGGGTACTGCGTCTGCGTATTCAGAA 300
OY 301 TACACCTACTTTTGCATGGGGGGAAGATAATGTATTAACAGACTTCAAGACCTTGGAGCC 360
    |||||||
DB 301 TACACCTACTTTTGCATGGGGGGAAGATAATGTATTAACAGACTTCAAGACCTTGGAGCC 360
OY 361 CGGCATTTCTATGACACTGACACTGACATGACATGCTGTAGTTTGAACCTTGTGTTGAG 420
    |||||||
DB 361 CGGCATTTCTATGACACTGACACTGACATGACATGCTGTAGTTTGAACCTTGTGTTGAG 420
OY 421 CCGTGATTTGTGACACTGTGCGACGCCCTCGAAGAACTTTTATAGTCAAGCAGAGACAA 480
    |||||||
DB 421 CCGTGATTTGTGACACTGTGCGACGCCCTCGAAGAACTTTTATAGTCAAGCAGAGACAA 480
OY 481 GAGGAGATTAAGTGGGCGACCTCCCGGTGCGATCACCTGCATCTTGAGAGACAGACTTGTG 540
    |||||||
DB 481 GAGGAGATTAAGTGGGCGACCTCCCGGTGCGATCACCTGCATCTTGAGAGACAGACTTGTG 540
OY 541 AAGTCAGAGCTGTACACATTAATCTCAACAGCTTGTGAGATTCGATGATGATGAGA 600
    |||||||
DB 541 AAGTCAGAGCTGTACACATTAATCTCAACAGCTTGTGAGATTCGATGATGATGAGA 600
OY 601 AGAAAGATTTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCCATGTTGTA 660
    |||||||
DB 601 AGAAAGATTTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCCATGTTGTA 660
OY 661 ATTGAAGACTTTGAGTCTCTCACTTACCCGTTGCGTACCCCACTGTCACAAGCCTCTCTG 720
    |||||||
DB 661 ATTGAAGACTTTGAGTCTCTCACTTACCCGTTGCGTACCCCACTGTCACAAGCCTCTCTG 720
OY 721 AATATTCCTGTTTACCCCGCAAGATTTTACAGGTATACATGCGAGAGTCTCTTGGCGAG 780
    |||||||
DB 721 AATATTCCTGTTTACCCCGCAAGATTTTACAGGTATACATGCGAGAGTCTCTTGGCGAG 780
OY 781 GAGGAAGCCCAAGTATCTGTGACTTTCAGAGANTCAGATTTTTCAGAGGCCAATTTCAAG 840
    |||||||
DB 781 GAGGAAGCCCAAGTATCTGTGACTTTCAGAGANTCAGATTTTTCAGAGGCCAATTTCAAG 840
OY 841 GCACTTCAACTTACTAGGAATGATGATCAATAAAACCACTGCTGCTGATGATGATGAT 900
    |||||||
DB 841 GCACTTCAACTTACTAGGAATGATGATCAATAAAACCACTGCTGCTGATGATGATGAT 900
OY 901 TCAATACAGACTTTTCTATACAGCTGAGAGATGCTTCAAGCTGATGATGATGATGAT 960
    |||||||
DB 901 TCAATACAGACTTTTCTATACAGCTGAGAGATGCTTCAAGCTGATGATGATGATGAT 960
OY 961 GATTCTGAGTACAAAGCTTACTCAAAAGACTGACGCTTGATGATTAAGAGAGACTGCG 1020
    |||||||

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|||||
Db GATTCGAGTACAAAGCCTACTCCAAAGACTGCAGCTTGAGATATAAAGAGAGCATGCG 1020
Qy 1021 GTCCCTTTGAAAATTAAGGACACACAAAGAAAGAGAGCTACTTACCACGATATA 1080
Db 1021 GTCCCTTTGAAAATTAAGGACACACAAAGAAAGAGAGCTACTTACCACGATATA 1080
Qy 1081 CCTGGGAGATGTTCTCTCAGTTCAATTTTACTGCTGTTGAATCCGAGCATTTCT 1140
Db 1081 CCTGGGAGATGTTCTCTCAGTTCAATTTTACTGCTGTTGAATCCGAGCATTTCT 1140
Qy 1141 AAAAAGCATTTTTCGAGCCCTTGAGACTATACAGAGACAGTGTGAAAAAGCGCAGG 1200
Db 1141 AAAAAGCATTTTTCGAGCCCTTGAGACTATACAGAGACAGTGTGAAAAAGCGCAGG 1200
Qy 1201 CTACAGAGCTGTGAGTAACAAAGGGCAGCCGATTAATAGCCGTTTCTACGAAATGCC 1260
Db 1201 CTACAGAGCTGTGAGTAACAAAGGGCAGCCGATTAATAGCCGTTTCTACGAAATGCC 1260
Qy 1261 TGTGCTGCTGTTGTTGATCTCTCTCCCTTCCTTCCTTCGACACACACACTAGTCTC 1320
Db 1261 TGTGCTGCTGTTGTTGATCTCTCTCCCTTCCTTCCTTCGACACACACACTAGTCTC 1320
Qy 1321 CTGCTCGAATCTTCTTAACCTTCAACCCAGACATATTCGTGCAAGCTCAAGTTTA 1380
Db 1321 CTGCTCGAATCTTCTTAACCTTCAACCCAGACATATTCGTGCAAGCTCAAGTTTA 1380
Qy 1381 TTTTCAACCCAGAAACCTCATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCCACA 1440
Db 1381 TTTTCAACCCAGAAACCTCATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCCACA 1440
Qy 1441 ACAGAGGTTCTGCGAAGGAGATATGTACAGAGCTGCTGCTGCTGTTGTTGTTCTCTCAGTT 1500
Db 1441 ACAGAGGTTCTGCGAAGGAGATATGTACAGAGCTGCTGCTGCTGTTGTTGTTCTCTCAGTT 1500
Qy 1501 CTTGAGCCAAACATACATGATCCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1560
Db 1501 CTTGAGCCAAACATACATGATCCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1560
Qy 1561 TCCATCTCTCTCGAACAACAATTTCTTCCATTCACAGATGACCCCTCATTCGCCATC 1620
Db 1561 TCCATCTCTCTCGAACAACAATTTCTTCCATTCACAGATGACCCCTCATTCGCCATC 1620
Qy 1621 ATAAATGTGGGTCCAGGAACCGGATAGCCCGTTTATTTGGTCTCTACACATAGAGAG 1680
Db 1621 ATAAATGTGGGTCCAGGAACCGGATAGCCCGTTTATTTGGTCTCTACACATAGAGAG 1680
Qy 1681 AAATCTCAAGAACACACCCAGATGAAATTTTGAAGCAATGTGTTTGTGCTGC 1740
Db 1681 AAATCTCAAGAACACACCCAGATGAAATTTTGAAGCAATGTGTTTGTGCTGC 1740
Qy 1741 AGGCATTAAGGATAGGATTAATCTTCTTCAAGAAAGCTCAGACATTTCTTAAAGATGGG 1800
Db 1741 AGGCATTAAGGATAGGATTAATCTTCTTCAAGAAAGCTCAGACATTTCTTAAAGATGGG 1800
Qy 1801 ATCTTAATCATCTAAAGGTTTCTTCTTCAAGAGATGCTCTGTTGGGAGAGAGAGGCC 1860
Db 1801 ATCTTAATCATCTAAAGGTTTCTTCTTCAAGAGATGCTCTGTTGGGAGAGAGAGGCC 1860
Qy 1798 ATCTTAATCATCTAAAGGTTTCTTCTTCAAGAGATGCTCTGTTGGGAGAGAGAGGCC 1857
Db 1798 ATCTTAATCATCTAAAGGTTTCTTCTTCAAGAGATGCTCTGTTGGGAGAGAGAGGCC 1857
Qy 1861 CCAGCAAAAGTATGTACAGACACATCCAGCTTCAATGCGCCAGAGTGGCGAAGATCCTC 1920
Db 1861 CCAGCAAAAGTATGTACAGACACATCCAGCTTCAATGCGCCAGAGTGGCGAAGATCCTC 1920
Qy 1921 CTCCAGGAGAAAGGCGCATTTATGTTGTGAGATGCAAAAGATATGCCCAAGATGTA 1980
Db 1921 CTCCAGGAGAAAGGCGCATTTATGTTGTGAGATGCAAAAGATATGCCCAAGATGTA 1980
Qy 1918 CATGATGCCCTTGTGCAAAATTAAGCAAGAGGTTGAGTTGAAAAACTAAGACAAATG 2040
Db 1918 CATGATGCCCTTGTGCAAAATTAAGCAAGAGGTTGAGTTGAAAAACTAAGACAAATG 2040
Qy 2041 AAAACCTGCGCATTTTAAAGAGAAAAAGCTTACAGATATTTGTCATATA 2097
Db 2041 AAAACCTGCGCATTTTAAAGAGAAAAAGCTTACAGATATTTGTCATATA 2097

Db 2038 AAAACCTGCGCATTTTAAAGAGAAAAAGCTTACAGATATTTGTCATATA 2094
RESULT 6
US-09-371-347-47
; Sequence 47, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE.
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 50/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 2093
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-47
Query Match 99.1%; Score 2077.4; DB 12; Length 2093;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2092; Conservative 0; Mismatches 1; Indels 4; Gaps 1;
Qy 1 ATGAGAGAGTTCTGTACTATATGCTACAGACGAGGAGGCAAGGCCATCGCAGAA 60
Db 1 ATGAGAGAGTTCTGTACTATATGCTACACACGAGGAGGCAAGGCCATCGCAGAA 60
Qy 61 GAAATATGTGACCAAGCTGTGTACATGATGATTTTGTGAGATCTTCACTGTATTAAGTAA 120
Db 61 GAAATATGTGACCAAGCTGTGTACATGATGATTTTGTGAGATCTTCACTGTATTAAGTAA 120
Qy 121 TCCGATTAATGACCTTAAACCAACAGCTCTCTTGTGTTGTGTTCTTACACAG 180
Db 121 TCCGATTAATGACCTTAAACCAACAGCTCTCTTGTGTTGTGTTCTTACACAG 180
Qy 181 GGCACCGGAGACCCACCCGACACAGCCGCAAGTTGTTAAGGAATACAGAACCAACA 240
Db 181 GGCACCGGAGACCCACCCGACACAGCCGCAAGTTGTTAAGGAATACAGAACCAACA 240
Qy 241 CTGCGGTTGATTTCTTGTCTACCTGCGGTATGGGTTACTGGGTCTCGGTATTCAGAA 300
Db 241 CTGCGGTTGATTTCTTGTCTACCTGCGGTATGGGTTACTGGGTCTCGGTATTCAGAA 300
Qy 301 TACACCTACTTTTGCATATGGGGGAAAGATTAATGATTAACGACTTCAAGAGCTTGGAGCC 360
Db 301 TACACCTACTTTTGCATATGGGGGAAAGATTAATGATTAACGACTTCAAGAGCTTGGAGCC 360
Qy 361 CGGCAATTTATGACACTGACATGCAATGCACTGTGTGTTGAACTTGTGGTTAG 420
Db 361 CGGCAATTTATGACACTGACATGCAATGCACTGTGTGTTGAACTTGTGGTTAG 420
Qy 421 CCGTGGATTTGTGAGACTGTGCGACGCTCAGAAAGCATTTTAAAGTCAAGAGAGACAA 480
Db 421 CCGTGGATTTGTGAGACTGTGCGACGCTCAGAAAGCATTTTAAAGTCAAGAGAGACAA 480
Qy 481 GAGGAGATTAAGTGGGCACTCCCGGTGGCATACCTGCTTCTTGAAGACACAGCTTGG 540
Db 481 GAGGAGATTAAGTGGGCACTCCCGGTGGCATACCTGCTTCTTGAAGACACAGCTTGG 540
Qy 541 AAGTCAGAGCTCTACATTAATCTCAAGTGCAGAGCTTCTGAGATTGATGATTCAGAGA 600
Db 541 AAGTCAGAGCTCTACATTAATCTCAAGTGCAGAGCTTCTGAGATTGATGATTCAGAGA 600
Qy 601 AGAAGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCAATGTTGTA 660
Db 601 AGAAGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCAATGTTGTA 660

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Db      601 AGAAGATTCGTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCAATGTGTGA 660
QY      661 ATTGAAGACTTGTAGTCTCTCACTTACCCGTTGGGTACCCCACTCTCACAGCTCTCTG 720
        |||||
Db      661 ATTGAAGACTTGTAGTCTCTCACTTACCCGTTGGGTACCCCACTCTCACAGCTCTCTG 720
QY      721 AATATTCTGTGTTTACCCCAAGATATTTACAGGTATCATCTGACAGAGTCTCTGGCCAG 780
        |||||
Db      721 AATATTCTGTGTTTACCCCAAGATATTTACAGGTATCATCTGACAGAGTCTCTGGCCAG 780
QY      781 GAGGAAAGCCAGTATCTGTGACTTACAGAGATCCAGTTTTCAGAGTGGCAATTTCAAG 840
        |||||
Db      781 GAGGAAAGCCAGTATCTGTGACTTACAGAGATCCAGTTTTCAGAGTGGCAATTTCAAG 840
QY      841 GCAGTTCACCTACTACGATATGATGCAATTAACACACCTCTGCTGTGATTAATTTGACAT 900
        |||||
Db      841 GCAGTTCACCTACTACGATATGATGCAATTAACACACCTCTGCTGTGATTAATTTGACAT 900
QY      901 TCAATATACAGACTTTTCCATACGAGCTGAGATGCTTACGCTGATCTGCCCTAACAT 960
        |||||
Db      901 TCAATATACAGACTTTTCCATACGAGCTGAGATGCTTACGCTGATCTGCCCTAACAT 960
QY      961 GATTCGAGTCAAGAGCTTACTCCAAAGACTGACAGCTTGAAGATTAAGAGACAGCTGC 1020
        |||||
Db      961 GATTCGAGTCAAGAGCTTACTCCAAAGACTGACAGCTTGAAGATTAAGAGACAGCTGC 1020
QY      1021 GTCTTTTGAATAAAGGACAGACAAAGAAAGAGAGTACCTTACCCAGCATATA 1080
        |||||
Db      1021 GTCTTTTGAATAAAGGACAGACAAAGAAAGAGAGTACCTTACCCAGCATATA 1080
QY      1081 CCTGGGGATGTTCTCTCAGTTCAATTTTACCTGTGTCTTGAATCCGAGCAATTCCT 1140
        |||||
Db      1081 CCTGGGGATGTTCTCTCAGTTCAATTTTACCTGTGTCTTGAATCCGAGCAATTCCT 1140
QY      1141 AAAAGGATTTTTCGAGACCTTGTGACTTACAGAGTGAAGAGTGAAGAGGACAGG 1200
        |||||
Db      1141 AAAAGGATTTTTCGAGACCTTGTGACTTACAGAGTGAAGAGTGAAGAGGACAGG 1200
QY      1201 CTACAGAGCTGTGAGTAAACAGAGGAGGAGCGATTAAGCCGTTTGTACGAGATGCC 1260
        |||||
Db      1201 CTACAGAGCTGTGAGTAAACAGAGGAGGAGCGATTAAGCCGTTTGTACGAGATGCC 1260
QY      1261 TGTGCTGCTGTGTGATCTCTCTCGCTTCCCTTCTTGGCAGCCACACTCAGTCTC 1320
        |||||
Db      1261 TGTGCTGCTGTGTGATCTCTCTCGCTTCCCTTCTTGGCAGCCACACTCAGTCTC 1320
QY      1321 CTGCTCGAATCTTCTTAACTTCAACCAAGACCATATGCTGTGCAAGCTCAGTTTA 1380
        |||||
Db      1321 CTGCTCGAATCTTCTTAACTTCAACCAAGACCATATGCTGTGCAAGCTCAGTTTA 1380
QY      1381 TTTCAAGCAGGAAAGCTCATTGTTGTCTTCAACATTTGGAATTTCTGTACTGCCACA 1440
        |||||
Db      1381 TTTCAAGCAGGAAAGCTCATTGTTGTCTTCAACATTTGGAATTTCTGTACTGCCACA 1440
QY      1441 ACAGAGTTCGCGGAAGGAGTATGTACAGGCTGCGCTTGTGCTTGTGCTTCACTT 1500
        |||||
Db      1441 ACAGAGTTCGCGGAAGGAGTATGTACAGGCTGCGCTTGTGCTTGTGCTTCACTT 1500
QY      1501 CTTCAGCCAAACATACATGATCCCATAGAGACAGCGGAAAGCCCTGCTCTAAGATA 1560
        |||||
Db      1501 CTTCAGCCAAACATACATGATCCCATAGAGACAGCGGAAAGCCCTGCTCTAAGATA 1560
QY      1561 TGCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCATCCCATC 1620
        |||||
Db      1561 TGCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCATCCCATC 1620
QY      1621 ATATATGTGTGTCAGAGAACCGGATACCCCGTTTATTTGGTCTTCAACATAGAGAG 1680
        |||||
Db      1621 ATATATGTGTGTCAGAGAACCGGATACCCCGTTTATTTGGTCTTCAACATAGAGAG 1680
QY      1681 AAATCTCAGAGAACACACAGATGGAATTTTGGAGAAATGTGTTTGGTGGCTGC 1740
        |||||
Db      1681 AAATCTCAGAGAACACACAGATGGAATTTTGGAGAAATGTGTTTGGTGGCTGC 1740
QY      1677 AAATCTCAGAGAACACACAGATGGAATTTTGGAGAAATGTGTTTGGTGGCTGC 1736

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QY      1741 AGCATAAGAGATAGGATTAATATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGG 1800
        |||||
Db      1737 AGCATAAGAGATAGGATTAATATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGG 1796
        |||||
QY      1801 ATCTTAATCATCTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGGAGCC 1860
        |||||
Db      1797 ATCTTAATCATCTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGGAGCC 1856
        |||||
QY      1861 CCAGCAAGATATGTCAAGACACATCCAGCTTCAATGGCCAGCAGAGTGGCGAATCCTC 1920
        |||||
Db      1857 CCAGCAAGATATGTCAAGACACATCCAGCTTCAATGGCCAGCAGAGTGGCGAATCCTC 1916
        |||||
QY      1921 CTCAGAGAAAGGCGCATATTATGTGTGAGATGCAAGAAATATGAGGCAAGATGTA 1980
        |||||
Db      1917 CTCAGAGAAAGGCGCATATTATTTATGTGTGAGATGCAAGAAATATGAGGCAAGATGTA 1976
        |||||
QY      1981 CATGATGCCCTTGTCAATAATATAGCAAGAGCTTGGAGTTGAATACTAGAACATG 2040
        |||||
Db      1977 CATGATGCCCTTGTCAATAATATAGCAAGAGCTTGGAGTTGAATACTAGAACATG 2036
        |||||
QY      2041 AAACCTTGGCCACTTTTAAAGAGAAAGAGCTTACCTTCAGAGATTTTGGTCATTA 2097
        |||||
Db      2037 AAACCTTGGCCACTTTTAAAGAGAAAGAGCTTACCTTCAGAGATTTTGGTCATTA 2093
        |||||

RESULT 7
US-09-909-567B-38
; Sequence 38, Application US/0909567B
; Publication No. US2003002257A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto A.
; APPLICANT: Nair, Manoj
; APPLICANT: Chen, Seiyu
; TITLE OR INVENTION: Compositions and Methods Relating to Lung Specific Genes
; FILE REFERENCE: DEX-0214
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,834
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patencin version 3.1
; SEQ ID NO 38
; LENGTH: 2475
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1001)..(1001)
; OTHER INFORMATION: a, c, g or t
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1011)..(1011)
; OTHER INFORMATION: a, c, g or t
US-09-909-567B-38

Query Match      8.3%; Score 174.4; DB 12; Length 2475;
Best Local Similarity 96.7%; Pred. No. 1.4e-44;
Matches 178; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY      510 ATCACTGATCTCTTGTAGAGACAGACTTGTGAAGTCAAGAGCTGTACATTTGAATCTCA 569
        |||||
Db      1 ATCACTGATCTCTGTAGAGACAGACTTGTGAAGTCAAGAGCTGTACATTTGAATCTCA 60
        |||||
QY      570 AGTCAGCTTCTGAGATTCGATGATTCAGAGAAAGAGATTCGAGTTTGAAGCAAAA 629
        |||||
Db      61 AGTCAGCTTCTGAGATTCGATGATTCAGAGAAAGAGATTCGAGTTTGAAGCAAAA 120
        |||||
QY      630 TGCAGTGAACAGCAACCAATCATGTTGTAATGAAGACTTTGAGTCTCATTACCCG 689
        |||||
Db      121 TGCAGTGAACAGCAACCAATCATGTTGTAATGAAGACTTTGAGTCTCATTACCCG 180
        |||||
QY      690 TTCG 693

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Db 181 TTGC 184

RESULT 8
US-09-917-800A-1351

Sequence 1351, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 1351
LENGTH: 1872
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 E01524
US-09-917-800A-1351

Query Match 4.2%; Score 88.6; DB 11; Length 1872;
Best Local Similarity 56.2%; Pred. No. 4.9e-17;
Matches 222; Conservative 0; Mismatches 149; Indels 24; Gaps 2;

1588 TTCCACTTACGAGATGACCCCTCAATCCCATCATTAATGTTGGTCCAGAACCCGCATTA 1647
1387 TTCCCGTTCCCTTTCAAGTCCACACACCTGTATCATGTGGCCCGGCACTGGATT 1446
1648 GCCCGTTATTGGTTCCTTACACATAGAGAAATCCCAAGAACACACCCAGATGA 1707
1447 GCCCTTTTATGGGCTTATCCAGAGACAGCTGGCTCGAGAGCAAGCAAGGAGG-- 1504
1708 AATTTTGGACATGTGTTGTTTGGCTCAGGCAATAGAGATAGGATATATCTATTTC 1767
1505 ---TGGGAGAGACGCTGCTATATCTATGCTCGCGGCTCGATAGAGATATCTGTAC 1560
1768 AGAAAAGACTAGACATTTCTTAAGCATGGGATCTTAAGTCAATCTAAAGTTTCCTTC 1827
1561 CGTGAAGACTAGCCCGCTTCCACAGAGAGCGGTGCTCAGCGAGCTTAATGTGGCTTT 1620
1828 TCAAGAGATGCTCTGTTGGGAGAGAGAACCCCAAGAGATATGTACAGACAATC 1887
1621 TCCCG-----GGAGCAGGCCCAAGGTCTATGTTCAGAGACCTTCG 1662
1888 CAGCTTACAGCCAGAGGTGGCAGATCTCTCCAGAGAGAACGCCATATTATATGTCG 1947

Db 1663 AAGAGAGACGAGAACACCTGTGTGAAGCTGATCCAGAGAGCGGTGCCCATCTATGTG 1722
1948 TGTGAGATGCAAGATATGCGCAAGATGTACA 1982
1723 TCGGGGATGCTCGAATATATGGCCAAAGATGTGCA 1757

RESULT 9
US-09-917-800A-1397

Sequence 1397, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 1397
LENGTH: 2401
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 M10068
US-09-917-800A-1397

Query Match 4.2%; Score 88.6; DB 11; Length 2401;
Best Local Similarity 56.2%; Pred. No. 5.8e-17;
Matches 222; Conservative 0; Mismatches 149; Indels 24; Gaps 2;

1588 TTCCACTTACGAGATGACCCCTCAATCCCATCATTAATGTTGGTCCAGAACCCGCATTA 1647
1556 TTCCCGTTCCCTTTCAAGTCCACACACCTGTATCATGTGGCCCGGCACTGGATT 1615
1648 GCCCGTTATTGGTTCCTTACACATAGAGAAATCCCAAGAACACACCCAGATGA 1707
1616 GCCCTTTTATGGGCTTATCCAGAGACAGCTGGCTTCGAGAGCAAGCAAGGAGG-- 1673
1708 AATTTTGGACATGTGTTGTTTGGCTCAGGCAATAGAGATAGGATATATCTATTTC 1767
1674 ---TGGGAGAGACGCTGCTATATCTATGCTGCGGCTCGATAGAGATATCTGTAC 1729
1768 AGAAAAGACTAGACATTTCTTAAGCATGGGATCTTAAGTCAATCTAAAGTTTCCTTC 1827
1730 CGTGAAGACTAGCCCGCTTCCACAGAGAGCGGTGCTCAGCGAGCTTAATGTGGCTTT 1789
1828 TCAAGAGATGCTCTGTTGGGAGAGAGAACCCCAAGAGATATGTACAGACAATC 1887
1790 TCCCG-----GGAGCAGGCCCAAGGTCTATGTTCAGAGACCTTCG 1831

QY 1888 CAGCTTCATGCGCAGAGTGGCGAGAAATCTCTCCAGAGAACGCCATATTATGTG 1947
DB 1832 AAGAGAGACAGGAGAACCTGTGTGAAGCTATCCACAGCGCGTCCACATCTATGTG 1891
QY 1948 TGTGGAGATGCAAGAATATGATGCAAGATGTACA 1982
DB 1892 TCGCGGGAGTCTCGAATAATATGCGCAAGAATGTGCA 1926

RESULT 10
US-09-783-590-1364
Sequence 1364, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: FO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1364
LENGTH: 101
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (2)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (62)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-1364

Query Match
Best Local Similarity 95.0%; Score 83.8; DB 11; Length 101;
Matches 96; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1673 ATAGAGAACTCCAGAACACACCCAGATGAATTTGGACCAATGTGTTGTTT 1732
DB 1 ANAGAGAACTCCAGAACACACCCAGATGAATTTGGACCAATGTGTTGTTT 60
QY 1733 TTGGCTGAGCATTAAGATAGG-ATTATCTATTTCAGAA 1772
DB 61 TTGGCTGAGCATTAAGATAGG-ATTATCTATTTCAGAA 101

RESULT 11
US-09-294-093B-4842
Sequence 4842, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:
APPLICANT: Lalugudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL Program
SEQ ID NO 4842

LENGTH: 298
TYPE: DNA
ORGANISM: Zee mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incycle ID No. US20010051335A1 700355168H1
US-09-294-093B-4842

Query Match
Best Local Similarity 58.0%; Score 61; DB 10; Length 298;
Matches 148; Conservative 0; Mismatches 100; Indels 7; Gaps 2;
QY 1587 TTTCCACTTACAGATGACCCCTCAATCCCATCATATATGTTGGTCCAGAACCCGCAT 1646
DB 46 TTCAAGTTACCTGTCGACCCATCCATCCGATTCATATGATTTGTCCTGGGACAGC-T 104
QY 1647 AGCCCGTTTATGGTTCCTACACATAGAGAACTCCAGAACACCCAGATGG 1706
DB 105 GGCCTCTTTTAAAGGCTTTCTTCAGAGAAAGTTAGCATGAAACAT-----CTGAGC 158
QY 1707 AATTTTGGACATGTGTTGTTTGGTCTGACGATTAAGATAGGATTTATCTATT 1766
DB 159 AGACTGGGACCTTCAATCTTTCTTGGATGACAGAACCGTAATATGACATATA 218
QY 1767 CAGAAAAGCTCAGACATTTCTTAAAGATGGATCTTAACATCTAAAGTTCTT 1826
DB 219 TGAAGATGAGCTCAAACTTCTTGGAGAGGGGGCGCTTTCTGACTAATTTGTCATT 278
QY 1827 CTCACAGATGCTCC 1841
DB 279 CTCTCGGGAAGGCC 293

RESULT 12
US-09-822-849A-278
Sequence 278, Application US/09822849A
Patent No. US20020045170A1
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakari
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 278
LENGTH: 2470
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-849A-278

Query Match
Best Local Similarity 55.6%; Score 59.6; DB 10; Length 2470;
Matches 138; Conservative 0; Mismatches 104; Indels 6; Gaps 1;
QY 1588 TTCCACTTACAGATGACCCCTCAATCCCATCATATATGTTGGTCCAGAACCCGCATA 1647
DB 1615 TTCCGCGCTTCAAGGCCACCCAGCGCTGTCATTCATGTTGGGCCCCGCGACCGCGTG 1674
QY 1648 GCCCGTTTATGGTTCCTCAACATAGAGAACTCCAGAACACACACACCCAGATGA 1707
DB 1675 GCACCTTCATAGCTTCATCCAGAGGGGCGCTGGCTGCGACAGGCGACAGGAGG- 1732

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2003, 09:58:39 ; Search time 89.0595 Seconds

(without alignments)
7221.032 Million cell updates/sec

Title: US-09-371-347A-41

Perfect score: 2097

Sequence: 1 atgaggaagttctgtact.....ttcagatatgtgtacataa 2097

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_NA:*
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5: /cgn2_6/ptodata/1/lna/PCUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2095.4	99.9	3259	4	US-09-318-448-23
2	386.4	18.4	390	4	US-08-905-223-71
3	63.6	3.0	4353	2	US-08-365-486A-18
4	63.6	3.0	4353	4	US-08-880-342-18
5	63.6	3.0	4780	2	US-08-365-486A-20
6	63.6	3.0	4780	3	US-09-123-708-3
7	63.6	3.0	4780	3	US-09-123-708-3
8	63.6	3.0	4780	4	US-08-880-342-20
9	57.2	2.7	5057	2	US-08-365-486A-12
10	57.2	2.7	5057	4	US-08-880-342-12
11	57.2	2.7	5108	1	US-07-642-002-1
12	53.6	2.5	1863	4	US-09-627-216A-13
13	52.8	2.5	1890	4	US-09-134-001C-1557
14	50.2	2.4	1448	4	US-08-936-165A-113
15	49.2	2.3	4145	4	US-09-302-620B-82
16	46.2	2.2	7218	1	US-08-232-463-14
17	46	2.2	4206	4	US-09-302-620B-81
18	44	2.1	307	4	US-09-172-711-24
19	43.4	2.1	7218	1	US-08-232-463-14
20	40.6	1.9	382	4	US-08-976-259-78
21	39.6	1.9	4041	1	US-08-147-812-4
22	39.6	1.9	4110	3	US-09-123-708-1
23	39.6	1.9	4110	3	US-09-123-624-1
24	39.6	1.9	4165	1	US-08-147-812-6
25	36.6	1.7	3701	1	US-08-553-279-1
26	36.6	1.7	43546	4	US-09-146-053-6
27	36	1.7	4089	1	US-07-908-245-1

28	36	1.7	4097	3	US-09-123-708-5	Sequence 5, Appl1
29	36	1.7	4097	4	US-09-123-624-5	Sequence 5, Appl1
30	35.4	1.7	1296	4	US-09-134-001C-1501	Sequence 1501, Ap
31	34.2	1.6	1569	1	US-08-680-726A-57	Sequence 57, Appl
32	34.2	1.6	1569	3	US-09-092-409-57	Sequence 57, Appl
33	34.2	1.6	10592	1	US-08-680-726A-51	Sequence 51, Appl
34	34.2	1.6	10592	1	US-08-680-726A-52	Sequence 52, Appl
35	34.2	1.6	10592	3	US-09-092-409-51	Sequence 51, Appl
36	34.2	1.6	10592	3	US-09-092-409-52	Sequence 52, Appl
37	34	1.6	2223	1	US-08-257-073-4	Sequence 4, Appl1
38	33.8	1.6	1702	1	US-08-261-822A-14	Sequence 14, Appl
39	33.8	1.6	1702	5	PCR-US95-0774A-14	Sequence 14, Appl
40	33.8	1.6	4146	1	US-08-261-822A-15	Sequence 15, Appl
41	33.8	1.6	4146	5	PCR-US95-0774A-15	Sequence 15, Appl
42	33.2	1.6	2277	1	US-08-676-974-2	Sequence 2, Appl1
43	33.2	1.6	2277	1	US-08-676-974-2	Sequence 2, Appl1
44	33.2	1.6	2277	2	US-09-098-487-2	Sequence 2, Appl1
45	32.6	1.6	2193	4	US-09-427-261-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1									
US-09-318-448-23									
Sequence 23, Application US/09318448									
Patent No. 6210950									
GENERAL INFORMATION:									
APPLICANT: Johnson, William G.									
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING									
FILE REFERENCE: 601-1-057									
CURRENT APPLICATION NUMBER: US/09/318,448									
CURRENT FILING DATE: 1999-05-25									
NUMBER OF SEQ ID NOS: 46									
SOFTWARE: PatentIn Ver. 2.0									
SEQ ID NO: 23									
LENGTH: 3259									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-09-318-448-23									
Query Match									
Best Local Similarity 99.9%: Score 2095.4; DB 4; Length 3259;									
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
OY	1	ATGAGGAGGTTCTGTACTATATATCTACACAGGAGGAGCAAGGCCATCGCAGAA	60						
DB	80	ATGAGGAGGTTCTGTACTATATATCTACACAGGAGGAGCAAGGCCATCGCAGAA	139						
OY	61	GAATATGTGACAGAGCTGTGTACATGGATTTTTCAGATCTTCACTATTAGTGA	120						
DB	140	GAATATGTGACAGAGCTGTGTACATGGATTTTTCAGATCTTCACTATTAGTGA	199						
OY	121	TCGGAATGATGACCTAAACGAAACAGCTCTCTGTGTGTGTCTACACG	180						
DB	200	TCGGAATGATGACCTAAACGAAACAGCTCTCTGTGTGTGTCTACACG	259						
OY	181	GGCAGCGAGACCCAGCCAGACAGCCGCAAGTTTGAAGGAATACAGAACCAACA	240						
DB	260	GGCAGCGAGACCCAGCCAGACAGCCGCAAGTTTGAAGGAATACAGAACCAACA	319						
OY	241	CTGCGGTTGATTTTCTGCTACCTCGGATATGCGTTACTGCTCGGTATTCAGAA	300						
DB	320	CTGCGGTTGATTTTCTGCTACCTCGGATATGCGTTACTGCTCGGTATTCAGAA	379						
OY	301	TACACCTCTTTTGAATGGGGGAAGATTAATGAACGACTCAAGAGCTTGAGCC	360						
DB	380	TACACCTCTTTTGAATGGGGGAAGATTAATGAACGACTCAAGAGCTTGAGCC	439						
OY	361	CGGATTTCTATGACACTGACATGCAATGACTGTAGTTTGAACCTTGCTGAG	420						

440 CGGATTTCTATGACACTGACATGACATGACTGTGTAGTTTGAACCTTGTGGTTGAC 499
421 CCGTGATTTGCTGACCTGTGCGCAGCCCTCAGAAAGCATTTTAGTGTACAGAGAGACAA 480
500 CCGTGATTTGCTGACCTGTGCGCAGCCCTCAGAAAGCATTTTAGTGTACAGAGAGACAA 559
481 GAGGAGATTAAGTGGCGCAGCTCCCGGTGGCATCCCTGCACTCTTGAGAGACAGACCTTGTG 540
560 GAGGAGATTAAGTGGCGCAGCTCCCGGTGGCATCCCTGCACTCTTGAGAGAGACAGACCTTGTG 619
541 AAGTCAGAGCTGTACACATGATGATCTCACTGACGCTTGTGAGATTTGATGATTCAGAGA 600
620 AAGTCAGAGCTGTACACATGATGATCTCACTGACGCTTGTGAGATTTGATGATTCAGAGA 679
601 AGAAGAGATTTCTGAGGTTTGAAGCAAAATGACAGAGACAGCAACCAATTCATTTGTTA 660
680 AGAAGAGATTTCTGAGGTTTGAAGCAAAATGACAGAGACAGCAACCAATTCATTTGTTA 739
661 ATTGAGAGCTTTGAGTCTCTCACTTACCCGTTGGTACCCGCTCTCAAGAGCTCTCTG 720
740 ATTGAGAGCTTTGAGTCTCTCACTTACCCGTTGGTACCCGCTCTCAAGAGCTCTCTG 799
721 AATATCTGTTTACCCCGAGAAATTTTACAGGATCTGTGAGAGATCTCTTGGCCAG 780
800 AATATCTGTTTACCCCGAGAAATTTTACAGGATCTGTGAGAGATCTCTTGGCCAG 859
781 GAGGAAGCCAGATATCTGTACTGTACAGATCCAGTTTTCAGAGTCCCAATTTCAAG 840
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841 GCAGTCAACTTACTAGCAATGATGCCATTAAGCACTCTGCTGTGATTTGACACTT 900
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901 TCAATACAGACTTTTCTATCAGCTGAGATGCTTACAGCTGATCTGCTTGAACGT 960
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961 GATTCTGAGTACAAAGCTCTCAAGAGCTGACGCTTGAAGATTAAGAGAGACACTGC 1020
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1021 GTCTTTTGAATTAAGGAGACACAAAGAGAGAGTACCTTACCCAGCATATA 1080
1100 GTCTTTTGAATTAAGGAGACACAAAGAGAGAGTACCTTACCCAGCATATA 1159
1081 CCTGCGGAGTGTCTCTCAGTTCATTTTACCTGCTGTCTTGAATCCGAGCATTTCT 1140
1160 CCTGCGGAGTGTCTCTCAGTTCATTTTACCTGCTGTCTTGAATCCGAGCATTTCT 1219
1141 AAAAAGCATTTTGGAGCCCTTGTGAGTATACAGTGAAGTGTGAAGAGCGCAGG 1200
1220 AAAAAGCATTTTGGAGCCCTTGTGAGTATACAGTGAAGTGTGAAGAGCGCAGG 1279
1201 CTACAGAGCTGTGACATTAAGGAGGAGGAGCCATTTATACCCGCTTGTGAGAGTGC 1260
1280 CTACAGAGCTGTGACATTAAGGAGGAGGAGCCATTTATACCCGCTTGTGAGAGTGC 1339
1261 TGTGCTGCTGTGTGATCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
1340 TGTGCTGCTGTGTGATCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1399
1321 CTGCTCGAATCTTCT 1380
1400 CTGCTCGAATCTTCT 1459
1381 TTTACCCAGGAAGCTTCATTTTGTCTCAACATTTGGAATTTGTCTACTGACACA 1440
1460 TTTACCCAGGAAGCTTCATTTTGTCTCAACATTTGGAATTTGTCTACTGACACA 1519
1441 ACAGAGGTTCTGCGGAGGAGTATGTACAGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 1500
1520 ACAGAGGTTCTGCGGAGGAGTATGTACAGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 1579

1501 CTTCAGCCAAATACATATGATCCATGATGAACAGACGCGGAGAAAGCCCTGCTCTAAGATA 1560
1580 CTTCAGCCAAATACATATGATCCATGATGAACAGACGCGGAGAAAGCCCTGCTCTAAGATA 1639
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1640 TCATCTCTCTCTGAGCAACAAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1699
1621 ATATGAGGCTCTGAGCAACCGGATAGCCCGCTTTTGTGGTCTCTCAACATAGAGAG 1680
1700 ATATGAGGCTCTGAGCAACCGGATAGCCCGCTTTTGTGGTCTCTCAACATAGAGAG 1759
1681 AAATCTCAAGAAACACACCCAGATGAATTTTGGACCAATGTGTTTGTGGCTGC 1740
1760 AAATCTCAAGAAACACACCCAGATGAATTTTGGACCAATGTGTTTGTGGCTGC 1819
1741 AGCATTAAGATAGGATTTATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGG 1800
1820 AGCATTAAGATAGGATTTATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGG 1879
1801 ATCTTAATCTATTAAGGTTTCTCTCTCAAGAGATCTCTCTGTTGGGAGAGAGAGCC 1860
1880 ATCTTAATCTATTAAGGTTTCTCTCTCAAGAGATCTCTCTGTTGGGAGAGAGAGCC 1939
1861 CCAGCAAAAGTATGTACAAAGACATCCAGCTTATGCGCAGAGAGTGGGAGATCTC 1920
1940 CCAGCAAAAGTATGTACAAAGACATCCAGCTTATGCGCAGAGAGTGGGAGATCTC 1999
1921 CTCCAGAGAAAGCGCATTTATTTATGTGTGTGAGATGCAAAAGATATGCGCAGAGATGA 1980
2000 CTCCAGAGAAAGCGCATTTATTTATGTGTGTGAGATGCAAAAGATATGCGCAGAGATGA 2059
1981 CATGATGCGCTTGTGCAAAATATTAAGCAAGAGTGTGAGTTGAAGAACTAAGAGCATG 2040
2060 CATGATGCGCTTGTGCAAAATATTAAGCAAGAGTGTGAGTTGAAGAACTAAGAGCATG 2119
2041 AAAACCTGCGCACTTTAAAGAGAAAGAGCTACCTTCAGATATTTGGTCATAA 2097
2120 AAAACCTGCGCACTTTAAAGAGAAAGAGCTACCTTCAGATATTTGGTCATAA 2176

RESULT 2
US-08-905-223-71
Sequence 71, Application US/08905223
Patent No. 622029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelien, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: DOUBLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: CDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo Sapiens
 TISSUE TYPE: Brain
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 289..357
 IDENTIFICATION METHOD: Von Heijne matrix
 OTHER INFORMATION: score 6.9
 OTHER INFORMATION: seq SLSLASHSVSC/SN
 US-08-905-223-71

Query Match 18.4%; Score 386.4; DB 4; Length 390;
 Best Local Similarity 99.7%; Pred. No. 1.7e-116;
 Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 1 AAGTACAAAGCCTACTCAAGAGCTGACCTGAAGATAAAGAGAGACACTGGCTCTTT 60
 DB 1028 TGAATAAAGCAGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1087
 61 TGAATAAAGCAGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 QY 1088 GATGTCCTCCAGTTCATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1147
 121 GATGTCCTCCAGTTCATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 1148 CATTTTGGAGCCCTTGTGACTATACAGTACAGTGTGTAAGAGCGAGGCTACAG 1207
 181 CATTTTGGAGCCCTTGTGACTATACAGTACAGTGTGTAAGAGCGAGGCTACAG 240
 QY 1208 AGCTGTCAGTAACAAGGGGCGAGGCGATTAAGCGCTTTGTACAGATGCTGTGCT 1267
 241 AGCTGTCAGTAACAAGGGGCGAGGCGATTAAGCGCTTTGTACAGATGCTGTGCT 300
 DB 1268 GCTTGTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1327
 301 GCTTGTGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 1328 AACATCTTCTTAACCTTCAACCCAGAC 1355
 361 AACATCTTCTTAACCTTCAACCCAGAC 388
 DB

RESULT 3
 US-08-365-486A-18
 Sequence 18, Application US/08365486A
 Patent No. 5834306
 GENERAL INFORMATION:
 APPLICANT: Webster, Keith A.
 APPLICANT: Bishopric, Nanette H.
 TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 TITLE OF INVENTION: Therapeutic Constructs
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/365,486A
 FILING DATE: 23-DEC-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 8255-0018
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4353 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al,
 INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..4305
 US-08-365-486A-18

Query Match 3.0%; Score 63.6; DB 2; Length 4353;
 Best Local Similarity 48.8%; Pred. No. 5.5e-10;
 Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

QY 1588 TTCCACTTACCAATACCCCTCAATCCCATATATGCTGGCTCAGAGACCGCAT 1647
 3715 TTCCACTTACCCGGAAGCCCAAGTCCCTGATCTGCTGACAGGACCGCAT 3774
 DB 1648 GCGCCGTTTATGTTGGTCTCAACAATPAGAGAACTCCAAACACCCAGATGGA 1707
 3775 GCGCCGTTTCCGAAGCTTCTGCGACACAGC---GCAATTGATATCCAAACCAAGAAAG 3831
 QY 1708 AATTGGAGCAATGCTGTTTGTGCTGCGAGCATPAGATAGGATTAATTC 1767
 3832 AACCCCTGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3891
 DB 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGAGATCTTAATCTTAAGGTTTCCTTC 1827
 3892 AGGAGAGAGACCTCGAGGCAAGAAAGGGGCTCTTCAAGAGCTGTACAGGCTTAC 3951
 QY 1828 TCAAGAGATGCTCTGTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1887
 3952 TCCC-----GGAGAGCAACAACCAAGAAAGTGCAGGACATCTTCG 3996
 DB 1888 CAGCTTCATGGCAGCAGGAGTGGAGAAATCTCTCCAGGAGAAAGGCAATATTATGTC 1947
 3997 CAGGAGCAGTGGCGGAGTGTGTACCGAGCCCTGAAGAGCAAGAGGCGCCCATATAC 4056
 QY 1948 TGTGAGATGCCAAGAATATGCCCCAAGATGTACATGATGCCCTTGTGCAATATTAAGC 2007
 4057 GTCTGTGGGAGCTCAGCATGCTGCTGATGCTCTCAAAAGCCATCCAGCCCATATGACC 4116
 DB 2008 AAGAGGTTGATTTGAAAACATAGAAAGCAATGAAACCTTGCCACTTTAAAGAAAGAA 2067
 4117 CAGCAGGGAGAGCTTCGCGAGAGAGCGCGGATTCATCAAGCCGAGATGAGGATGAC 4176
 QY 2068 AACGCTACCTTCAGATATTT 2089
 4177 AACGATACCATGAGATATTT 4198
 DB

RESULT 4
 US-08-880-342-18

```

: Sequence 18 Application US/08880342
: Patent No.6218179
:
: GENERAL INFORMATION:
: APPLICANT: Webster, Keith A.
: APPLICANT: Bishopric, Nanette H.
: APPLICANT: Murphy, Brian
: APPLICANT: Laderoute, Keith R.
: APPLICANT: Green, Christopher J.
: TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
: TITLE OF INVENTION: Therapeutic Constructs
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Avenue, Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/880,342
: FILING DATE: 23-JUN-1997
: CLASSIFICATION: 514
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/1995/00996
: FILING DATE: 13-NOV-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/365,486
: FILING DATE: 23-DEC-1994
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Sholtz, Charles K.
: REGISTRATION NUMBER: 38,615
: REFERENCE/DOCKET NUMBER: 8255-0018.30
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 324-0880
: TELEFAX: (415) 324-0960
:
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4353 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al,
: INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..4305
:
: US-08-880-342-18
:
: Query Match 3.0%; Score 63.6; DB 4; Length 4353;
: Best Local Similarity 48.8%; Pred. NO.5.5e-10;
: Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;
:
: Oy 1588 TTCGACTTACAGATGACCCCTCATATCCCATCAATAATAGTGGGTCACGAACCGGCATA 1647
: Db 3715 TTCCACCGCGCCCGGAAAGCCCAAGTCCCTGCAATCCCTGTGGACGACGACCGGCATT 3774
: Oy 1648 GCCCGCTTATTGGGCTTCATCAACATAGAGAGAGAAACTCCAAGAACACACCCAGATGA 1707
: Db 3775 GCCCGCTTCCCAAGACTCTGTGCAACAGCG--GCAATTGTATTCACACACAAAGAAATG 3831
:
: Oy 1708 AATTGGAGCAATGTGTTGTTTGGGCTGCAAGGCAATAGATATATCTATTC 1767
: Db 3832 AACCCCTGCCCATGTCTGTGCTTGGGCGCGGCAATCAAGATATATCTATTC 3891

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US-08-365-486A-20

Query Match 3.0%; Score 63.6; DB 2; Length 4780;

Best Local Similarity 48.8%; Pred. No. 5.9e-10;

Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

OY 1588 TTCACCTTACAGATGACCCCTCAATCCCATCATATGTTGGTGGACAGAACCGGCAAT 1647
 DB 4142 TTCACCTGCCCCGGGAACCCCAAGTCCCTCATCTCTGTTGACAGACCGGCAAT 4201
 OY 1648 GCCCGCTTATTTGGTCTTCTACACATAGAGAAACTCCAAAGAACACCCACATGGA 1707
 DB 4202 GCCCTTTCGGAAGCTTCTGGCAACAGCG--GCAATTTGATATCCAAACAAAGGAATG 4258
 OY 1708 AATTTTGAGCAATGTGTTTGTGCTGACGACATTAAGATTAAGGATTAATCTATTC 1767
 DB 4259 AACCCCTGCCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4318
 OY 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGGGATCTTAACATCTAAAGGTTTCCTTC 1827
 DB 4319 AGGGAAGAGACCTCGACGCGCAAGAAACAAGGGGCTTCAGAGAGCTGTACACGGCTTAC 4378
 OY 1828 TCAAGAGATGCTCTGTTGGGAGAGAGAACCCCAAGCAAGTATGTACAGACAAATC 1887
 DB 4379 TCCC-----GGGAGCGACAGCAAAACCAAGAAAGATGCTGACGAGCAATCCTG 4423
 OY 1888 CAGCTTCATGGCCAGAGTGCGAGAAATCCTCTCCAGAGACAGCGGCATATTATGTG 1947
 DB 4424 CAGAGACAGCTGGCGAGTCTGTATCCAGACGCTGAAGAGCAAGGGGCCACATATAC 4483
 OY 1948 TGTGAGATGCAAAAGATATGCGCAAGCATGTACATGATGACCTTGTGCAAAATTAATAC 2007
 DB 4484 GTCTGTGGGAGCTGACCATGCTGCTGATGTCTCAAGCCATCCAGGCAATCATGACC 4543
 OY 2008 AAAGAGTTGGATTGAAATACTAGAACGATGAACCCCTGSCCATTTAAAGAGAA 2067
 DB 4544 CAGCAGGGGAGACCTCTCGGCAAGAGACCGCGGCTATTCATGACCGCATGAGGATGAC 4603
 OY 2068 AACGCTACCTCAGGATATT 2089
 DB 4604 AACCATACCATGAGGATATT 4625

RESULT 6

US-09-123-708-3

Sequence 3, Application US/09123708

Patent No. 6146887

GENERAL INFORMATION:

APPLICANT: SCHRAEDER, Juergen

APPLICANT: GODECKE, Axel

TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC

FILE REFERENCE: 511169-2003

CURRENT APPLICATION NUMBER: US/09/123,708

CURRENT FILING DATE: 1998-07-28

EARLIER APPLICATION NUMBER: 08/553,503

EARLIER FILING DATE: 1996-03-01

EARLIER APPLICATION NUMBER: P4411402.8

EARLIER FILING DATE: 1994-03-31

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 4780

TYPE: DNA

ORGANISM: Cytomegalovirus

US-09-123-708-3

Query Match 3.0%; Score 63.6; DB 3; Length 4780;

Best Local Similarity 48.8%; Pred. No. 5.9e-10;

Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

OY 1588 TTCACCTTACAGATGACCCCTCAATCCCATCATATGTTGGTGGACAGAACCGGCAAT 1647
 DB 4142 TTCACCTGCCCCGGGAACCCCAAGTCCCTCATCTCTGTTGACAGACCGGCAAT 4201
 OY 1648 GCCCGCTTATTTGGTCTTCTACACATAGAGAAACTCCAAAGAACACCCACATGGA 1707
 DB 4202 GCCCTTTCGGAAGCTTCTGGCAACAGCG--GCAATTTGATATCCAAACAAAGGAATG 4258
 OY 1708 AATTTTGAGCAATGTGTTTGTGCTGACGACATTAAGATTAAGGATTAATCTATTC 1767
 DB 4259 AACCCCTGCCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4318
 OY 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGGGATCTTAACATCTAAAGGTTTCCTTC 1827
 DB 4319 AGGGAAGAGACCTCGACGCGCAAGAAACAAGGGGCTTCAGAGAGCTGTACACGGCTTAC 4378
 OY 1828 TCAAGAGATGCTCTGTTGGGAGAGAGAACCCCAAGCAAGTATGTACAGACAAATC 1887
 DB 4379 TCCC-----GGGAGCGACAGCAAAACCAAGAAAGATGCTGACGAGCAATCCTG 4423
 OY 1888 CAGCTTCATGGCCAGAGTGCGAGAAATCCTCTCCAGAGACAGCGGCATATTATGTG 1947
 DB 4424 CAGAGACAGCTGGCGAGTCTGTATCCAGACGCTGAAGAGCAAGGGGCCACATATAC 4483
 OY 1948 TGTGAGATGCAAAAGATATGCGCAAGCATGTACATGATGACCTTGTGCAAAATTAATAC 2007
 DB 4484 GTCTGTGGGAGCTGACCATGCTGCTGATGTCTCAAGCCATCCAGGCAATCATGACC 4543
 OY 2008 AAAGAGTTGGATTGAAATACTAGAACGATGAACCCCTGSCCATTTAAAGAGAA 2067
 DB 4544 CAGCAGGGGAGACCTCTCGGCAAGAGACCGCGGCTATTCATGACCGCATGAGGATGAC 4603
 OY 2068 AACGCTACCTCAGGATATT 2089
 DB 4604 AACCATACCATGAGGATATT 4625

RESULT 7

US-09-123-624-3

Sequence 3, Application US/09123624

Patent No. 6149936

GENERAL INFORMATION:

APPLICANT: SCHRAEDER, Juergen

APPLICANT: GODECKE, Axel

TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

FILE REFERENCE: 511169-2004

CURRENT APPLICATION NUMBER: US/09/123,624

CURRENT FILING DATE: 1998-07-28

PRIOR APPLICATION NUMBER: 08/553,503

PRIOR FILING DATE: 1996-03-01

PRIOR APPLICATION NUMBER: 4411402.8

PRIOR FILING DATE: 1994-03-31

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 4780

TYPE: DNA

ORGANISM: Homo sapiens

US-09-123-624-3

Query Match 3.0%; Score 63.6; DB 3; Length 4780;

Best Local Similarity 48.8%; Pred. No. 5.9e-10;

Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

OY 1588 TTCACCTTACAGATGACCCCTCAATCCCATCATATGTTGGTGGACAGAACCGGCAAT 1647
 DB 4142 TTCACCTGCCCCGGGAACCCCAAGTCCCTCATCTCTGTTGACAGACCGGCAAT 4201
 OY 1648 GCCCGCTTATTTGGTCTTCTACACATAGAGAAACTCCAAAGAACACCCACATGGA 1707
 DB 4202 GCCCTTTCGGAAGCTTCTGGCAACAGCG--GCAATTTGATATCCAAACAAAGGAATG 4258
 OY 1708 AATTTTGAGCAATGTGTTTGTGCTGACGACATTAAGATTAAGGATTAATCTATTC 1767
 DB 4259 AACCCCTGCCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4318
 OY 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGGGATCTTAACATCTAAAGGTTTCCTTC 1827
 DB 4319 AGGGAAGAGACCTCGACGCGCAAGAAACAAGGGGCTTCAGAGAGCTGTACACGGCTTAC 4378
 OY 1828 TCAAGAGATGCTCTGTTGGGAGAGAGAACCCCAAGCAAGTATGTACAGACAAATC 1887
 DB 4379 TCCC-----GGGAGCGACAGCAAAACCAAGAAAGATGCTGACGAGCAATCCTG 4423
 OY 1888 CAGCTTCATGGCCAGAGTGCGAGAAATCCTCTCCAGAGACAGCGGCATATTATGTG 1947
 DB 4424 CAGAGACAGCTGGCGAGTCTGTATCCAGACGCTGAAGAGCAAGGGGCCACATATAC 4483
 OY 1948 TGTGAGATGCAAAAGATATGCGCAAGCATGTACATGATGACCTTGTGCAAAATTAATAC 2007
 DB 4484 GTCTGTGGGAGCTGACCATGCTGCTGATGTCTCAAGCCATCCAGGCAATCATGACC 4543
 OY 2008 AAAGAGTTGGATTGAAATACTAGAACGATGAACCCCTGSCCATTTAAAGAGAA 2067
 DB 4544 CAGCAGGGGAGACCTCTCGGCAAGAGACCGCGGCTATTCATGACCGCATGAGGATGAC 4603
 OY 2068 AACGCTACCTCAGGATATT 2089
 DB 4604 AACCATACCATGAGGATATT 4625

Db	4259	AAACCTTCCCCCATGTGCTCTGTCTGGGTCCGGCCAAATCCAGATGATCATATATCTAC	4318
QY	1768	AGAAAAGAGCTCAGACATATTTCTCTTAAGCATGGGATCTTAACATCATTAAGGTTTCTCTTC	1827
Db	4319	AGGGAGAGACCTTCGACAGCCCAAGAACAGGGGGCTTCCACAGAGCTGTACACCGGCTTAC	4378
QY	1828	TCAAGAGATGCTCTGTGGGAGAGAGAACCCCGACGAAGTATGTTCAGACACAACTC	1887
Db	4379	TCCC-----GGAGCCGACACAACCCAAAGAGTACGTGCAGGACATCTCG	4423
QY	1888	CAGCTTCATGCGCCAGCAGGTGGCCAGAAATCTCTCCAGAGAAAGCGCATATTTATGTG	1947
Db	4424	CAGGAGCAGCTGGGGGAGTCTGTGTACCGACCTCGAAGAGAGCAAGGGGGCCACATATAC	4483
QY	1948	TGTGGAGATGCAAAGATATGCGCAAGGATGTACATGATGCCCTTGTGCCAATATATAAGC	2007
Db	4484	GTCTGTGGGGAGCGTACACCATGGCTGTGATGTCTCTCAAAAGCATTCAGCGCATATGACC	4543
QY	2008	AAAGAGGTGAGTGTGAAAAAAGCTGAAGCAATGAAAAACCTTGGCCACTTTTAAAGAAAGAA	2067
Db	4544	CAGCAGGGGGAAGCTCTCGCGCAGAGAGACCGCGCGTATTCATCAGCCGAGTATGAGGATGAC	4603
QY	2068	AAAGCTACCTTCAGGATATTT	2089
Db	4604	AACCGATCCATGAGATATTT	4625

RESULT 8
 US-08-880-342-20
 Sequence 20 Application US/08880342
 Patent No. 6218179
 GENERAL INFORMATION:
 APPLICANT: Webster, Keith A.
 APPLICANT: Bishopric, Nanette H.
 APPLICANT: Murphy, Brian
 APPLICANT: Laderoute, Keith R.
 APPLICANT: Green, Christopher J.
 TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 TITLE OF INVENTION: Therapeutic Constructs
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/880,342
 FILING DATE: 23-JUN-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/IB95/00996
 FILING DATE: 13-NOV-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/365,486
 FILING DATE: 23-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 8255-0018.30
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4780 base pairs
 TYPE: nucleic acid

```

? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? INDIVIDUAL ISOLATE: Human NOS-SN gene, Nakane, et al,
? INDIVIDUAL ISOLATE: FEBS Lett 316:175 (1993)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 431..4732
? US-08-880-342-20

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Query Match	3.0%;	Score 63.6;	DB 4;	Length 4780;
Best Local Similarity	48.8%;	Pred. No. 5.9e-10;		
Matches 245;	Conservative 0;	Mismatches 239;	Indels 18;	Gaps 2;

OY	1588	TTCCACTTACCAAGATGACCCTCATATCCCCATTAATGATGGGTGCAGGAACCGGCATA	1647
Db	4142	TTCCACCTGCCCGCAGAACCCCAGTCCTGATCCCTTGATGGACACGACCGGCATT	4201
OY	1648	GCCCCGTTTATTTGGGTCCTTACAACATGAGAAGAACTCCAAGAACACCCAGATGGA	1707
Db	4202	GCCCCCTTCCAGACCTTCTGGCACAGCG---GCAATTTGATATCCAAACAAAAGGAATG	4258
OY	1708	AATTTTGAGCATGTGTGTTTTTTTGGCTGCAGGCAATTAAGATAGGATTTATCTATTG	1767
Db	4259	AAACCCTGCCCCATGTCTCTGTCTTGCGGTGCGGCATATCCAGATGATCATTTCTTAG	4318
OY	1768	AGAAAGAGCTCAGACATTTCTTAAAGCATGGATCTTAACTCATCTAAGGTTTCCTTC	1827
Db	4319	AGGAGAGAGACCTTCGACAGGCCAACAAGGGGGCTTCAAGAGAGCTGTACACGGCTTAC	4378
OY	1828	TCAAGAGATGCTCTGTTGGGGAGGAGAACCCGACGAAGTATGTTCAGACAACTC	1887
Db	4379	TCCC-----GGAGCGMACAAACAAAGAATAGTGTACGAGACATCTGTG	4423
OY	1888	CAGCTTATATGSCACAGAGTGGCCAGATCTCTCCTCGAGGAACGGCCATATTATATGTG	1947
Db	4424	CAGAGACAGCTGGCGGAGTGTGTAGCCAGCCCTGAAGAGCAAGGGGCGCACATATAC	4483
OY	1948	TGTGAGATGCAAAAGATATGTGCCAAGATGTACATGTGCTTGTGCAATATATAGC	2007
Db	4484	GTCGTGGGGAGTCACCATGGCTGTGATGTCTCAAAGGCATTCACCGCATCATGACC	4543
OY	2008	AAAGAGTTGAGTTGAAAACTAGAGCAATGAAAAACCTGCGCATTCTTAAAGAGAA	2067
Db	4544	CAGCAGGGGAAGCTCTGGCGAGAGAGCGCGGCTATTATCATCACCGGATGAGGATGAC	4603
OY	2068	AAACGCTACCTTCAGGATATT	2089
Db	4604	AACCGATACCATGAGGATATT	4625

RESULT 9
US-08-365-486A-12
Sequence 12 Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: rat bnos cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 349..4638
US-08-365-486A-12
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Query Match      2.7%: Score 57.2; DB 2; Length 5057;
Best Local Similarity 48.0%: Pred. No. 7,6e-08;
Matches 241; Conservative 0; Mismatches 243; Indels 18; Gaps 2;
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QY 1588 TTCCACTTACGAGATGACCCCTCAATCCCATCATATATGCTGGCTCAGAGAACCGGCATA 1647
DB 4048 TTCACCTGCTCGAAGACCTTTCGCAACAGGAGGCTTCATCTGTTGGCCAGACACTGGCATC 4107
QY 1648 GCCCGTTATTGGGTTCTCTACATAGAGAAACTCCAAAGCAACACCAGATGGA 1707
DB 4108 GCACCTTCCGAAGCTTTCGCAACAGGAC---AATTGACATCCACACCAAGGAATG 4164
QY 1708 AATTTGGAGCAATGCTGTTGTTTGGCTCAGGCATTAAGGATTAAGGATTATCTATTC 1767
DB 4165 AATCGTGCCCATGCTGCTGCTCGGCTGTCGACATCCAAAGATAGATCATATCTAC 4224
QY 1768 AAAAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAACATCTTAAGGTTTCCTTC 1827
DB 4225 AGAGAGGAGACCTTCAGGCTAAGAACAAAGGCGCTTCAGAGAGCTGTACACTGCTAT 4284
QY 1828 TCAAGAGATGCTCTGTTGGGAGAGAGGCCCGCAAGAAATGATGTACAGCAACATC 1887
DB 4285 TCCCGGGAAC-----GGACAGGCGCAAGAAATATGTACAGGACGTGCTG 4329
QY 1888 CAGCTTCATGGCCAGAGGTGGCGAGAAATCTCTCTCCAGAGAACGCCATATTTATGTG 1947
DB 4330 CAGGAACAGCTGGGTGAGTCTGTATACCGCGCCCTGAAGAGAGAGAGCCACATTTAT 4389
QY 1948 TGTGAGATGCAAAAGATATGCGCCAAAGATGTACATGATCCCTGTGTGCAAAATATTAAC 2007
DB 4390 GTCTGTGGGAGCTTACCATGCGCGGCTGCTCTTAAGACCATCCAGGCAATATGAGAC 4449
QY 2008 AAAGAGTGTGAGTGAAGAAATAGAGCAATGAAGAAACCTGGCCACTTTAAAGAGAA 2067
DB 4450 CAGCAGGGAACCTCTCAGAGAGAGAGCGCTGCTGTTATCATAGCAGGCTGAGAGGTAC 4509
QY 2068 AAACGCTTACCTCAGATATTT 2089
DB 4510 AACCGGTACCGAGAGACATCT 4531
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RESULT 10
US-08-880-342-12

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Sequence 12, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: rat bnos cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 349..4638
US-08-880-342-12
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Query Match      2.7%: Score 57.2; DB 4; Length 5057;
Best Local Similarity 48.0%: Pred. No. 7,6e-08;
Matches 241; Conservative 0; Mismatches 243; Indels 18; Gaps 2;
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DB 4048 TTCACCTGCTCGAAGACCTTTCGCAACAGGAGGCTTCATCTGTTGGCCAGACACTGGCATC 4107
QY 1648 GCCCGTTATTGGGTTCTCTACATAGAGAAACTCCAAAGCAACACCAGATGGA 1707
DB 4108 GCACCTTCCGAAGCTTTCGCAACAGGAC---AATTGACATCCACACCAAGGAATG 4164
QY 1708 AATTTGGAGCAATGCTGTTGTTTGGCTCAGGCATTAAGGATTAAGGATTATCTATTC 1767
DB 4165 AATCGTGCCCATGCTGCTGCTCGGCTGTCGACATCCAAAGATAGATCATATCTAC 4224
QY 1768 AAAAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAACATCTTAAGGTTTCCTTC 1827
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: SEQUENCE CHARACTERISTICS:
: LENGTH: 1448 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
US-08-936-165A-113

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Query Match	2.48;	Score 50.2;	DB 4;	Length.1448;
Best Local Similarity	58.38;	Pred. No. 6.4e-06;		
Matches 88; Conservative	0;	Mismatches 63;	Indels 0;	Gaps 0;

OY 1339 ATTATATCTGTGAGATSCAAAGAATATATGGCCCAAGANGTACTATGATGCCCTTGTCGA 1998
 116 ATCTATATTTTGTGCGCATGAAAAATGTATGGCCCAAGATGTCCCATCAAGCCATTAAAGT 175
 Db

Oy 1959 ATATATAACCAAGAGGTGGAGTGAAGAAAACTAAGAACAATGAAACCCTGGCCACTTTA 2058
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QY      2059 AAAGAAGAAAACGCTACCTTCAGGATATTT 2089
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Db      236 AACACACAACACGCTATCAACGTGATGTT 266

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RESULT 15
US-09-302-620B-82
: Sequence 82, Application US/09302620B
: Patent No. 6331420
: GENERAL INFORMATION:
: APPLICANT: Wilson, C. Ron
: APPLICANT: Craft, David L.
: APPLICANT: Birch, Dudley
: APPLICANT: Eshoo, Mark
: APPLICANT: Madduri, Krishna M.
: APPLICANT: Cornett, Cathy A.
: APPLICANT: Brenner, Alfred A.
: APPLICANT: Tang, Maria
: APPLICANT: Loper, John C.
: APPLICANT: Gleeson, Martin
: TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
: TITLE OF INVENTION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
: TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
: TITLE OF INVENTION: RELATING THERETO
: FILE REFERENCE: 1010-16.seg
: CURRENT APPLICATION NUMBER: US/09/302,620B
: CURRENT FILING DATE: 1999-04-30
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 82
: LENGTH: 4145
: TYPE: DNA
: ORGANISM: Candida tropicalis
: US-09-302-620B-82

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Query Match	2.3%;	Score 49.2;	DB 4;	Length 4145.
Best Local Similarity	58.0%;	Pred. No. 2.8e-05;		
Matches 109; Conservative	0;	Mismatches 73;	Indels 6;	Gaps 1;

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Db 2387 TTTAAGTTGCCAAGAATCTCACACACCCAGTATCTTGATGTGGTCCACGGTACATGCTGT 2646

QY 1648 GGGCCGGTATTATGGGTGCTACACATGAGAGAGAAAGCTCCAAAGAACACACCCAGATGCA 1107
DB 2647 GCGCCATTGAGAGAGTTCCTGCT-----TGGAGAAAGAGTTCACACAGTCAAGAAATGCTGTC 2700

QY 1708 AATTTTGCAGCANTGTGCTTTTTCGCTGCAGGCATTAAGGATTTATCTATTC 1767
Db 2701 AATGTTGGCAAGACTTTTGTGTTTATGTTGTCAGAACTCCACGAGCACTTTTGTAC 2760

QY 1768 AGAAAAGA 1775
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Db 2761 AAGCAAGA 2768

Search completed: July 29, 2003, 13:07:17
Job time : 92.0595 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2003, 10:56:19 ; Search time 425.084 Seconds
(without alignments)
10177.082 Million cell updates/sec

Title: US-09-371-347a-43
Perfect score: 2097
Sequence: 1 atgagagagttctgtact.....ttcagatatgttgcataa 2097

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Published Applications_NA.*
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17: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2097	100.0	2097	12	US-09-371-347-43	Sequence 43, Appl
2	2095.4	99.9	2097	12	US-09-371-347-1	Sequence 1, Appl
3	2095.4	99.9	3259	12	US-09-371-347-24	Sequence 24, Appl
4	2093.8	99.8	2097	12	US-09-371-347-41	Sequence 41, Appl
5	2079.4	99.2	2097	12	US-09-371-347-45	Sequence 45, Appl
6	2077.4	99.1	2093	12	US-09-371-347-47	Sequence 47, Appl
7	174.4	8.3	2475	12	US-09-909-567B-38	Sequence 38, Appl
8	88.6	4.2	1872	11	US-09-917-800A-1351	Sequence 1351, Ap
9	88.6	4.2	2401	11	US-09-917-800A-1397	Sequence 1397, Ap
10	83.8	4.0	101	11	US-09-783-5590-1364	Sequence 1364, Ap
11	61	2.9	298	10	US-09-294-093B-4842	Sequence 4842, Ap
12	59.6	2.8	2470	10	US-09-822-849A-278	Sequence 278, App
13	58.4	2.8	230	10	US-09-923-876-2645	Sequence 2845, Ap
14	57.2	2.7	13508	8	US-08-781-986A-120	Sequence 120, App
15	56	2.7	2136	11	US-09-938-842A-803	Sequence 803, App
16	54.8	2.6	2403	11	US-09-880-107-3039	Sequence 3039, App

17	53.6	2.6	1863	10	US-09-765-873A-13	Sequence 13, Appl
18	52.2	2.5	411	10	US-09-925-299-440	Sequence 440, App
19	52.2	2.5	411	12	US-09-925-299-440	Sequence 440, App
20	50.6	2.4	2088	15	US-10-128-714-7234	Sequence 7234, App
21	50.2	2.4	1448	15	US-09-939-980-113	Sequence 113, App
22	49.2	2.3	1944	15	US-10-272-017A-4	Sequence 4, Appl
23	49.2	2.3	3037	10	US-09-911-781-10	Sequence 10, Appl
24	49.2	2.3	4145	10	US-09-911-781-3	Sequence 3, Appl
25	49.2	2.3	4145	12	US-09-976-800-82	Sequence 82, Appl
26	49.2	2.3	4145	15	US-10-138-838-82	Sequence 82, Appl
27	49.2	2.3	4145	15	US-10-139-031-82	Sequence 82, Appl
28	49.2	2.3	4145	15	US-10-138-905-82	Sequence 82, Appl
29	49.2	2.3	4145	15	US-10-138-916-82	Sequence 82, Appl
30	47.6	2.3	1791	11	US-09-778-319-1	Sequence 1, Appl
31	47.6	2.3	4957	15	US-10-201-213-1	Sequence 1, Appl
32	46.4	2.2	1845	15	US-10-128-714-1234	Sequence 1234, Ap
33	46.4	2.2	1845	15	US-10-128-714-2234	Sequence 2234, Ap
34	46.4	2.2	2145	15	US-10-128-714-6234	Sequence 6234, Ap
35	46.4	2.2	3845	15	US-10-128-714-234	Sequence 234, App
36	46.4	2.2	4145	15	US-10-128-714-5234	Sequence 5234, Ap
37	46	2.2	1944	15	US-10-272-017A-1	Sequence 1, Appl
38	46	2.2	4206	10	US-09-911-781-2	Sequence 2, Appl
39	46	2.2	4206	12	US-09-976-800-81	Sequence 81, Appl
40	46	2.2	4206	15	US-10-138-838-81	Sequence 81, Appl
41	46	2.2	4206	15	US-10-139-031-81	Sequence 81, Appl
42	46	2.2	4206	15	US-10-138-905-81	Sequence 81, Appl
43	46	2.2	4206	15	US-10-138-916-81	Sequence 81, Appl
44	46	2.2	640681	11	US-09-790-988-1	Sequence 1, Appl
45	42.4	2.0	413	12	US-09-918-995-32917	Sequence 32917, A

ALIGNMENTS

RESULT 1
US-09-371-347-43
Sequence 43, Application US/09371347
Publication NO. US20030082676A1
GENERAL INFORMATION:
APPLICANT: Roy A. Gravel et al.
TITLE OF INVENTION: HUMAN MENTIONINE SYNTHASE REDUCTASE;
TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371, 347
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/071,622
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/232,028
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 2097
TYPE: DNA
ORGANISM: Homo sapiens
US-09-371-347-43

Query Match 100.0%; Score 2097; DB 12; Length 2097;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	ATGAGAGGTTTGTGTTACTATATGCTACACAGGAGGACGCAAGGCATCGCAGAA	60
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DB	61	GAATGTCGACGACGCTGTCGATGATTTTTCGACATTCATATATAGTGA	120
OY	121	TCGATATGATGACCTAAACCGAAGCAGCTCTCTGTTGTTGTTGTTTACACG	180
DB	121	TCGATATGATGACCTAAACCGAAGCAGCTCTCTGTTGTTGTTGTTTACACG	180

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241 CTGCGGGTATTTCTTGTCTCACTGCGGTATGGGTGTACGGGTCTGGGTATTCGAA 300
241 CTGCGGGTATTTCTTGTCTCACTGCGGTATGGGTGTACGGGTCTGGGTATTCGAA 300
301 TACACCTACTTTTGGCAATGGGGGAGAAATATGATTAACGACTTCAAGAGCTTGAAGCC 360
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361 CGGCATTTCATATGACACTGGACATGCAATGATGCTGTAGCTTTAGAACTTGTGAG 420
361 CGGCATTTCATATGACACTGGACATGCAATGATGCTGTAGCTTTAGAACTTGTGAG 420
421 CCGTGAATGCTGGAGCTGTGGCCAGCCCTCAGAAAGCATTTTGTGTCACAGACAGCA 480
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481 GAGGATATAGTGGCCACCTCCCGGTGCACTCACTGCACTCTTGAAGACAGACTTGTG 540
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1081 CCGCGGAGATTTCTCTCAGCTTCAATTTTCTGCTGTGTTGAATCCGAGCAATTTCT 1140
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1141 AAAAAGGATTTTGGCGAGCCCTGTGAGCTATACAGTGCAGAGTGCAGAAAGGCGCAGG 1200
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1381 TTTTACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGGAATTTCTGTACTGCAACA 1440
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1501 CTTTACGCCAACAATATGATGATTCCTTCAATGAAAGACAGCGGAAACCCCTGCTCTAAGATA 1560
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1681 AATCTCAAGAACACACCCAGATGGAATTTTGGAGCAATGTGTTTGTGCTCTGC 1740
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RESULT 2

US-09-371-347-1

; Sequence 1, Application US/09371347

; Publication No. US20030082676A1

; GENERAL INFORMATION:

; APPLICANT: Roy A. Gravel et al.

; TITLE OF INVENTION: HUMAN METHYLONLINE SYNTHASE REDUCTASE:

; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE

; TITLE OF INVENTION: DEFECTS CARDIOVASCULAR DISEASE, AND CANCER

; FILE REFERENCE: 50004/003003

; CURRENT APPLICATION NUMBER: US/09/371, 347

; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: 60/071,622

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: 09/232,028

; PRIOR FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2097
TYPE: DNA
ORGANISM: Homo sapiens
US-09-371-347-1

Query Match 99.9%; Score 2095.4; DB 12; Length 2097;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 901 TCAATATACAGACTTTCTTATACGCTTGAGATGCCCTTACGCGTATCTGCCCTAACAGT 960
QY 961 GATTCGTGAGTACAAAGCCTCTCCAAAGACCTGTAAGATTAAGAGACACTGC 1020
DB 961 GATTCGTGAGTACAAAGCCTCTCCAAAGACCTGTAAGATTAAGAGACACTGC 1020
QY 1021 GTCCCTTTGAAATTAAGGACACAAAGAGAGGCTTACCTTACCCAGCATTA 1080
DB 1021 GTCCCTTTGAAATTAAGGACACAAAGAGAGGCTTACCTTACCCAGCATTA 1080
QY 1081 CCTGGGAGTGTCTCTCAGCTTCAATTTTACCTGTGTCTTGAATTCAGCAATTCCT 1140
DB 1081 CCTGGGAGTGTCTCTCAGCTTCAATTTTACCTGTGTCTTGAATTCAGCAATTCCT 1140
QY 1141 AAAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTGCAGTGTGAAGAGCGCAGG 1200
DB 1141 AAAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTGCAGTGTGAAGAGCGCAGG 1200
QY 1201 CTACAGAGCTGTGACATTAACAAAGGAGCGCATTTATAGCGGCTTGTACAGATGCC 1260
DB 1201 CTACAGAGCTGTGACATTAACAAAGGAGCGCATTTATAGCGGCTTGTGTACAGATGCC 1260
QY 1261 TGTGCTCTCTTGTGATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
DB 1261 TGTGCTCTCTTGTGATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
QY 1321 CTGCTCGAATCTTCTTAACTTCAACCCAGACCATATTGCTGTGCAAGCTCAAGTTA 1380
DB 1321 CTGCTCGAATCTTCTTAACTTCAACCCAGACCATATTGCTGTGCAAGCTCAAGTTA 1380
QY 1381 TTTACCCAGGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTACTAGCCACA 1440
DB 1381 TTTACCCAGGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTACTAGCCACA 1440
QY 1441 ACAGAGTTTCTGCGAAGGAGATGTACAGGCTGCTGCTGCTTGTGTTGCTTCACTT 1500
DB 1441 ACAGAGTTTCTGCGAAGGAGATGTACAGGCTGCTGCTGCTTGTGTTGCTTCACTT 1500
QY 1501 CTTGAGCCAAACATCATGATCCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1560
DB 1501 CTTGAGCCAAACATCATGATCCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1560
QY 1561 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCATTC 1620
DB 1561 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCATTC 1620
QY 1621 ATATGTGTGCTCAGAAACCGGATAGCCCGTTTATTTGGTCTTCAACATAGAGAG 1680
DB 1621 ATATGTGTGCTCAGAAACCGGATAGCCCGTTTATTTGGTCTTCAACATAGAGAG 1680
QY 1681 AATCTCAGAAACACACCGAGATGGAATTTGAGGAATTTGTTTGGTGGC 1740
DB 1681 AATCTCAGAAACACACCGAGATGGAATTTGAGGAATTTGTTTGGTGGC 1740
QY 1741 AGGCAATGAGATGAGGATTAATCTATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGG 1800
DB 1741 AGGCAATGAGATGAGGATTAATCTATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGG 1800
QY 1801 ATCTTAATCATCTTAAGGTTTCTTCTCAGAGATGCTCTGTTGGGAGAGAGAACCC 1860
DB 1801 ATCTTAATCATCTTAAGGTTTCTTCTCAGAGATGCTCTGTTGGGAGAGAGAACCC 1860
QY 1861 CCAGCAAGATATGTACAGACACATCCAGCTTCAATGGCAGAGAGTGGCAATTCCTC 1920
DB 1861 CCAGCAAGATATGTACAGACACATCCAGCTTCAATGGCAGAGAGTGGCAATTCCTC 1920
QY 1921 CTCCAGAGAAAGGCGCATATTTATGTGTGAGATGCAAGAAATATGGCCAAGATGTA 1980
DB 1921 CTCCAGAGAAAGGCGCATATTTATGTGTGAGATGCAAGAAATATGGCCAAGATGTA 1980
QY 1981 CATGATGCCCTTGTCAATTAATTAAGCAAAAGGTTGAGTTGAAAACCTAGAACATG 2040
DB 1981 CATGATGCCCTTGTCAATTAATTAAGCAAAAGGTTGAGTTGAAAACCTAGAACATG 2040

Db 1981 CATGATGCCCTTGTGCAATATATAGCAAGAGTTGAGTTGAAAACTAGAGCAATG 2040
QY 2041 AAAACCTGGCCCTTTAAAGAAAGAAAAAGCTACTTATGATATTTGGTATTA 2097
Db 2041 AAAACCTGGCCCTTTAAAGAAAGAAAAAGCTACTTATGATATTTGGTATTA 2097

RESULT 3

US-09-371-347-24
; Sequence 24, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 3259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-24

Query Match 99.9%; Score 2095.4; DB 12; Length 3259;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAGGTTCTCTTACTATATCTACACAGAGGAGCAAGGCCATCCGAGAA 60
Db 80 ATGAGAGGTTCTCTTACTATATCTACACAGAGGAGCAAGGCCATCCGAGAA 139
QY 61 GAATGTGTGACAGAGTGTGTACATGATTTTGTGAGATCTTACATATTTGTGAA 120
Db 140 GAATGTGTGACAGAGTGTGTACATGATTTTGTGAGATCTTACATATTTGTGAA 199
QY 121 TCCGATTAAGTATGACCTAAAAACCGAACAGCTCTTGTGTGTGTTCTTCAACG 180
Db 200 TCCGATTAAGTATGACCTAAAAACCGAACAGCTCTTGTGTGTGTTCTTCAACG 259
QY 181 GGCACCGAGAGCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
Db 260 GGCACCGAGAGCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 319
QY 241 CTGCGGTTGATTTCTTGTCACTGTGGTATGGGTACTGGGTCTGGTATTCAGAA 300
Db 320 CTGCGGTTGATTTCTTGTCTACCTCGGTATGGGTACTGGGTCTGGTATTCAGAA 379
QY 301 TACACCTACTTTTGCATGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGGAGCC 360
Db 380 TACACCTACTTTTGCATGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGGAGCC 439
QY 361 CGGATTTCTATGACACTGACATGACAGATGACTGTGAGTTTGAAGACTTGGTTGAG 420
Db 440 CGGATTTCTATGACACTGACATGACAGATGACTGTGAGTTTGAAGACTTGGTTGAG 499
QY 421 CCGTGATTTGTTGACTGTGCGAGCCCTCAGAAAGCTTTTATGATCAAGAGAGACAA 480
Db 500 CCGTGATTTGTTGACTGTGCGAGCCCTCAGAAAGCTTTTATGATCAAGAGAGACAA 559
QY 481 GAGAGATTAAGTGGCGACTCCCGTGCGATCACCCTGATCCTTGAGAGACAGACTGTS 540
Db 560 GAGAGATTAAGTGGCGACTCCCGTGCGATCACCCTGATCCTTGAGAGACAGACTGTS 619
QY 541 AAGTCAGAGCTGTACACATTTGAATTCACAGTCTTCTGAGATTGATGATTCAGA 600

Db 620 AAGTCAGAGCTGTACACATTTGAATTCACAGTCTTCTGAGATTGATGATTCAGA 679
QY 601 AGAAGATTTCTGAGTTTGAAGCAAAATGACAGTAAAGCAACCAATCAATGTTGTA 660
Db 680 AGAAGATTTCTGAGTTTGAAGCAAAATGACAGTAAAGCAACCAATCAATGTTGTA 739
QY 661 ATTGAAGACTTTGAGTCTTCACTTACCCGTGGGTACCCCACTCTCAGAACGCTCTG 720
Db 740 ATTGAAGACTTTGAGTCTTCACTTACCCGTGGGTACCCCACTCTCAGAACGCTCTG 799
QY 721 AATATTCCTGTTTACCCCAAGATTAATTACAGTATCACTGTGAGAGATCTTGGCCAG 780
Db 800 AATATTCCTGTTTACCCCAAGATTAATTACAGTATCACTGTGAGAGATCTTGGCCAG 859
QY 781 GAGGAAGCCAGTATCTGTGACTTACAGAGATTCAGTTTCAAGTGGCAATTTGAAG 840
Db 860 GAGGAAGCCAGTATCTGTGACTTACAGAGATTCAGTTTCAAGTGGCAATTTGAAG 919
QY 841 GCAGTTCAACTTACTGCAATGATGCGATTAACCACTCTGCTGTAGATTTGACAT 900
Db 920 GCAGTTCAACTTACTGCAATGATGCGATTAACCACTCTGCTGTAGATTTGACAT 979
QY 901 TCAATATGACAGCTTTCTATCAGCTGAGATGCTTACGCTGATCTGCCCTAACGT 960
Db 980 TCAATATGACAGCTTTCTATCAGCTGAGATGCTTACGCTGATCTGCCCTAACGT 1039
QY 961 GATTCGAGTACAAAGCCTTACTCCAAAGACTGCAAGCTTGAAGATTAAGAGAGCACT 1020
Db 1040 GATTCGAGTACAAAGCCTTACTCCAAAGACTGCAAGCTTGAAGATTAAGAGAGCACT 1099
QY 1021 GTTCCTTTTGAATAAAGGACAGACACAAAGAAAGAGAGCTTACCTTACCCAGCATTA 1080
Db 1100 GTTCCTTTTGAATAAAGGACAGACACAAAGAAAGAGAGCTTACCTTACCCAGCATTA 1159
QY 1081 CCTGGGGATGTTCTCTCAGTTCATTTTACCCTGCTGTGAATCCGAGCAATTCCT 1140
Db 1160 CCTGGGGATGTTCTCTCAGTTCATTTTACCCTGCTGTGAATCCGAGCAATTCCT 1219
QY 1141 AAAAAGCAATTTTTCGAGCCCTTGTGAGTATACAGTGAAGTGAAGAGGCGAGG 1200
Db 1220 AAAAAGCAATTTTTCGAGCCCTTGTGAGTATACAGTGAAGTGAAGAGGCGAGG 1279
QY 1201 CTACAGAGCTGTGAGTAAACAGAGGCGAGCGATTAATAGCCGCTTTGTACGAGATGCC 1260
Db 1280 CTACAGAGCTGTGAGTAAACAGAGGCGAGCGATTAATAGCCGCTTTGTACGAGATGCC 1339
QY 1261 TGTGCTGCTGTTGATCTCTCTGCTGCTTCCCTTCTTCCAGCCACCACTAGTCTC 1320
Db 1340 TGTGCTGCTGTTGATCTCTCTGCTGCTTCCCTTCTTCCAGCCACCACTAGTCTC 1399
QY 1321 CTGCTGCAACATCTTCTTAACTTCAACCCAGACCATATTTGCTGCAAGCTCAAGTTTA 1380
Db 1400 CTGCTGCAACATCTTCTTAACTTCAACCCAGACCATATTTGCTGCAAGCTCAAGTTTA 1459
QY 1381 TTTACACCGAGAAAGCTCCATTTTGTCTTCAACATTTGGAATTTGTCTACTGCCACA 1440
Db 1460 TTTACACCGAGAAAGCTCCATTTTGTCTTCAACATTTGGAATTTGTCTACTGCCACA 1519
QY 1441 ACAGAGTTCTGCGGAAGGAGTATGTACAGGCTGGCGCTGCTGTTGCTTCACTT 1500
Db 1520 ACAGAGTTCTGCGGAAGGAGTATGTACAGGCTGGCGCTGCTGTTGCTTCACTT 1579
QY 1501 CTTCAGCCAAACATATCATGATCCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1560
Db 1580 CTTCAGCCAAACATATCATGATCCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1639
QY 1561 TTCATCTCTCTGCAACAACAATTTCTTCACTTACCAAGATGACCCCTCAATCCCATC 1620
Db 1640 TTCATCTCTCTGCAACAACAATTTCTTCACTTACCAAGATGACCCCTCAATCCCATC 1699
QY 1621 AATATGTTGGTCTCAGGAAACCGGATAGCCCGTTTATTTGGTCTCTTCAACATTAAGAG 1680
Db 1700 AATATGTTGGTCTCAGGAAACCGGATAGCCCGTTTATTTGGTCTCTTCAACATTAAGAG 1759

QY	1681	AAACTCCAAAGAACACACACCCAGATGGAAATTTTGAGCAATGTGTGTTTGTGCTGC	1740
Db	1760	AAACTCCAAAGAACACACCCAGATGGAAATTTTGAGCAATGTGTGTTTGTGCTGC	1819
QY	1741	AGGCATTAAGGTAGGGATTATCTATTGAGAAAAGAGTCAGACATTTTCCTTAACATGGG	1800
Db	1820	AGGCATTAAGGTAGGGATTATCTATTGAGAAAAGAGTCAGACATTTTCCTTAACATGGG	1879
QY	1801	ATCTTAACATCATCTAAAGGTTTCCCTTCACAGAGATCTCTGTGGGGAGAGAAAGCC	1860
Db	1880	ATCTTAACATCATCTAAAGGTTTCCCTTCACAGAGATCTCTGTGGGGAGAGAAAGCC	1939
QY	1861	CCAGCAAAGTATGTACAAAGACACATCCAGCTTATGCGCAGCAGGTGGCGAGATCCTC	1920
Db	1940	CCAGCAAAGTATGTACAAAGACACATCCAGCTTATGCGCAGCAGGTGGCGAGATCCTC	1999
QY	1921	CTCCAGAGAAAGCGCCATATTTATGTGTGGAGATGCAAGAAATATGGCCAAAGATGTA	1980
Db	2000	CTCCAGAGAAAGCGCCATATTTATGTGTGGAGATGCAAGAAATATGGCCAAAGATGTA	2059
QY	1981	CATGATGCCCTTGTCAAATTAATTAAGCAAGAGGTTGGATTTGAAAACTAGAAGCATG	2040
Db	2060	CATGATGCCCTTGTCAAATTAATTAAGCAAGAGGTTGGATTTGAAAACTAGAAGCATG	2119
QY	2041	AAAAACCTGGCCACTTTAAAAAGAAAGAAACGCTACTTACAGATATTTGGTCTATA	2097
Db	2120	AAAAACCTGGCCACTTTAAAAAGAAAGAAACGCTACTTACAGATATTTGGTCTATA	2176

RESULT 4
US-09-371-347-41
; Sequence 41, Application US/09371347
; Publication No. US20030082676A1

```

:  APPLICATION: Roy A. Gravel et al.
:  TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
:  TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF
:  TITLE OF INVENTION: DEFECTS/CARDIOVASCULAR DISEASE, AND CANCER
:  FILE REFERENCE: 50004/003003
:  CURRENT APPLICATION NUMBER: US/09/371,347
:  PRIOR FILING DATE: 1999-08-10
:  PRIOR APPLICATION NUMBER: 60/071,622
:  PRIOR FILING DATE: 1998-01-16
:  PRIOR APPLICATION NUMBER: 09/222,028
:  PRIOR FILING DATE: 1999-01-15
:  NUMBER OF SEO ID NOS: 51
:  SOFTWARE: FastSeq for Windows Version 4.0
:  SEO ID NO 41
:  LENGTH: 2097
:  TYPE: DNA
:  ORGANISM: Homo sapiens
:  IS-09-371-347-41

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Query Match	99.88;	Score 2093.8;	DB 12;	Length 2097;
Best Local Similarity	99.98;	Pred. No. 0;		
Matches 2095; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	I	ATGAGGAGGTTTCTGTTACTATATGCTACACAGCAGGACGCGAAAGGCCATCGCAGAA	60
Db	1	ATGAGGAGGTTCTGTTACTATATGCTACACAGCAGGACGCGAAAGGCCATCGCAGAA	60
QY	61	GAAATGCTGAGCACAAGCTGTGCTACATGGAATTTCTGCAGATCTTCCACTATATTAGGAA	120
Db	61	GAAATATGTGACACAAGCTGTGTGCTACATGGAATTTCTGCAGATCTTCACTGATTATTGAA	120
QY	121	TCCGATTAAGTATGACCTAAAAACCGAAACAGACTCTCTGTTGTTGTGTTCACACAG	180
Db	121	TCCGATTAAGTATGACCTAAAAACCGAAACAGACTCTCTGTTGTTGTGTTCACACAG	180
QY	181	GGCACCGGAGACCCACCCGACACAGCCCGCAGTTTGTTAAGGAATTCAGAACCAACA	240
Db	181	GGCACCGGAGACCCACCCGACACAGCCCGCAGTTTGTTAAGGAATTCAGAACCAACA	240

QY	241	CTGCGGGTATATTTCTTTTGTCTACCTCGGGTATGGGTTACTG6GTCTGGGTATTCAGAA	300
Db	241	CTGCGGGTATATTTCTTTTGTCTACCTCGGGTATGGGTTACTG6GTCTGGGTATTCAGAA	300
QY	301	TACACCTACCTTTTGCAATGGGGGAAGATAAATTGAATAAAGCATTCAGAGCTTGAGACC	360
Db	301	TACACCTACCTTTTGCAATGGGGGAAGATAAATTGAATAAAGCATTCAGAGCTTGAGACC	360
QY	361	CGGCATTTCTATGACACCTGGACATGACAGATGACTGTGTAGTGTAGAACTTGTGGTTGAG	420
Db	361	CGGCATTTCTATGACACCTGGACATGACAGATGACTGTGTAGTGTAGAACTTGTGGTTGAG	420
QY	421	CCGCGGATTTCTGAGACTCTGCGCCACGCCCTCACAAACATTTTAAAGTCAACGACGAGACAA	480
Db	421	CCGCGGATTTCTGAGACTCTGCGCCACGCCCTCACAAACATTTTAAAGTCAACGACGAGACAA	480
QY	481	GAGAGATTAAGTGGCGACATCCCGGTGGCATGACCTGCATCCCTTGAAGACAGACTTGTG	540
Db	481	GAGAGATTAAGTGGCGACATCCCGGTGGCATGACCTGCATCCCTTGAAGACAGACTTGTG	540
QY	541	AAGTCACAGCTGCTACACATTTGAATCTCAAGTCGAGCTTCTAGATTTGAGATTCACGA	600
Db	541	AAGTCACAGCTGCTACACATTTGAATCTCAAGTCGAGCTTCTAGATTTGAGATTCACGA	600
QY	601	AGAAAGATTTCTAGAGTTTGAAGCAAAATGCAGTAAACAGACAAATCCAAATTTGTGA	660
Db	601	AGAAAGATTTCTAGAGTTTGAAGCAAAATGCAGTAAACAGACAAATCCAAATTTGTGA	660
QY	661	ATTGAAAGCTTTGAGTCTCACTTACCCTGTCGGTACCCCACTCTCAACAAAGCTCTGTG	720
Db	661	ATTGAAAGCTTTGAGTCTCACTTACCCTGTCGGTACCCCACTCTCAACAAAGCTCTGTG	720
QY	721	AATATTCCTGGTTTACCCCGAATTTTAAAGGTACATCTGACAGAGTCTCTTGGCCAG	780
Db	721	AATATTCCTGGTTTACCCCGAATTTTAAAGGTACATCTGACAGAGTCTCTTGGCCAG	780
QY	781	GAGGAAAGCCCAAGTATCTGTGACTTACAGAGATTCACAGTTTTCAGGTGCAATTTCAAG	840
Db	781	GAGGAAAGCCCAAGTATCTGTGACTTACAGAGATTCACAGTTTTCAGGTGCAATTTCAAG	840
QY	841	GCAGTTCACCTACTACTACGAATGATGCCATTAATAAACACACTCTGCTGGTAGAATTTGACATT	900
Db	841	GCAGTTCACCTACTACTACGAATGATGCCATTAATAAACACACTCTGCTGGTAGAATTTGACATT	900
QY	901	TCAATATCACACTTTTCTATCAGCTGGAGATGCTTACGGTGAATCGCCCTTAACGT	960
Db	901	TCAATATCACACTTTTCTATCAGCTGGAGATGCTTACGGTGAATCGCCCTTAACGT	960
QY	961	GATTCTGAGGTACAAAGCCTACTCCAAAGACTGACCTTGAAGATTAAGACAGACACTGC	1020
Db	961	GATTCTGAGGTACAAAGCCTACTCCAAAGACTGACCTTGAAGATTAAGACAGACACTGC	1020
QY	1021	GTCCTTTTGAATAATAAAGGACAGACAAAGAAAGAAAGAGATACCTTACCCAGCATTA	1080
Db	1021	GTCCTTTTGAATAATAAAGGACAGACAAAGAAAGAAAGAGATACCTTACCCAGCATTA	1080
QY	1081	CTTGCGGGATGTCTCTCCAGTTCAATTTTACCCTGGTGTCTTGAATCCGAGCAATTCCT	1140
Db	1081	CTTGCGGGATGTCTCTCCAGTTCAATTTTACCCTGGTGTCTTGAATCCGAGCAATTCCT	1140
QY	1141	AAAAAGCATTTTTCGACGCCCTTGGAGCTATACCAAGTGAAGTGTAAAGGCGCAGG	1200
Db	1141	AAAAAGCATTTTTCGACGCCCTTGGAGCTATACCAAGTGAAGTGTAAAGGCGCAGG	1200
QY	1201	CTACAGAGCTGTGACAGTAAACCAAGGGGAGCCGATTATAGCCGGTTTGTACGAGATCC	1260
Db	1201	CTACAGAGCTGTGACAGTAAACCAAGGGGAGCCGATTATAGCCGGTTTGTACGAGATCC	1260
QY	1261	TGTGCTGTCTTGTGGATCTCTCTCCGCTTCTTCCCTTCTTGGCAGCCACACTCACTCACTC	1320
Db	1261	TGTGCTGTCTTGTGGATCTCTCTCCGCTTCTTCCCTTCTTGGCAGCCACACTCACTCACTC	1320

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QY 1321 CTGCTCGACATCTTCCCTAACTCAACCCAGACCATATTCGTGTCAGCTCAAGTTA 1380
    |||||||
Db 1321 CTGCTCGACATCTTCCCTAACTCAACCCAGACCATATTCGTGTCAGCTCAAGTTA 1380
QY 1381 TTTACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGAATTTGTCTACTGCCACA 1440
    |||||||
Db 1381 TTTACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGAATTTGTCTACTGCCACA 1440
QY 1441 ACAGAGGTTCTGGGAGGAGGTATGTACAGGCTGGGCGCTGTGGTGGTCTCACTT 1500
    |||||||
Db 1441 ACAGAGGTTCTGGGAGGAGGTATGTACAGGCTGGGCGCTGTGGTGGTCTCACTT 1500
QY 1501 CTTCAGCCAAACATACATGCATCCCATGAACAGACAGCGGAAAGCCCTGGCTCTCAAGTA 1560
    |||||||
Db 1501 CTTCAGCCAAACATACATGCATCCCATGAACAGACAGCGGAAAGCCCTGGCTCTCAAGTA 1560
QY 1561 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC 1620
    |||||||
Db 1561 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC 1620
QY 1621 ATATGTGGGTGTCAGAACCCGCGATAGCCCGTTTATTTGGTCTTCAACATAGAGAG 1680
    |||||||
Db 1621 ATATGTGGGTGTCAGAACCCGCGATAGCCCGTTTATTTGGTCTTCAACATAGAGAG 1680
QY 1681 AAACCTCAAGAACACACCCAGATGAAATTTTGGAGCAATGTGGTTTGTGGTGC 1740
    |||||||
Db 1681 AAACCTCAAGAACACACCCAGATGAAATTTTGGAGCAATGTGGTTTGTGGTGC 1740
QY 1741 AGGATTAAGATAGGAGTATCTATTCAGAAAAGAGCTCAGACATTTCTTAAACATGGG 1800
    |||||||
Db 1741 AGGATTAAGATAGGAGTATCTATTCAGAAAAGAGCTCAGACATTTCTTAAACATGGG 1800
QY 1801 ATCTTAATCTATCAAAAGTTTCTCTTCAAGAGATGCTCTGTGGGAGAGAGAAACC 1860
    |||||||
Db 1801 ATCTTAATCTATCAAAAGTTTCTCTTCAAGAGATGCTCTGTGGGAGAGAGAAACC 1860
QY 1861 CCACCAAAAGTATGTACAAAGACACATCCAGCTCATGGCCAGAGTGGCAGATCTCTC 1920
    |||||||
Db 1861 CCACCAAAAGTATGTACAAAGACACATCCAGCTCATGGCCAGAGTGGCAGATCTCTC 1920
QY 1921 CTCGAGGAGAAAGGCGCATTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
    |||||||
Db 1921 CTCGAGGAGAAAGGCGCATTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
QY 1981 CATGATGCCCTTGTGCAAAATATTAAGCAAAAGAGTTGAGTTGAAAACTGAAGCAATG 2040
    |||||||
Db 1981 CATGATGCCCTTGTGCAAAATATTAAGCAAAAGAGTTGAGTTGAAAACTGAAGCAATG 2040
QY 2041 AAAACCCCTGGCCACTTTAAAAAGAGAAAAAGCTACCTTCAGGATTTTGTCTATAA 2097
    |||||||
Db 2041 AAAACCCCTGGCCACTTTAAAAAGAGAAAAAGCTACCTTCAGGATTTTGTCTATAA 2097

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: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-371-347-45
Query Match 99.2%; Score 2079.4; DB 12; Length 2094;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 ATGAGAGAGTTTCTGTACTATATGCTACACAGACAGGACAGGCAAGGCCATGCGCAGAA 60
    |||||||
Db 1 ATGAGAGAGTTTCTGTACTATATGCTACACAGACAGGACAGGCAAGGCCATGCGCAGAA 60
QY 61 GAAATGTGTGAGCAAGCTGTGTACATGATTTTCTGCAGATCTTCACTATATTAGGAA 120
    |||||||
Db 61 GAAATGTGTGAGCAAGCTGTGTACATGATTTTCTGCAGATCTTCACTATATTAGGAA 120
QY 121 TCCGATTAAGTATGACCTTAAACCAGAAACAGCTCTCTTGTGTGTGTGTGTGTACACG 180
    |||||||
Db 121 TCCGATTAAGTATGACCTTAAACCAGAAACAGCTCTCTTGTGTGTGTGTGTGTACACG 180
QY 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
    |||||||
Db 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
QY 241 CTGCGCGTTGATTTCTTGTCTCACCTGGATGAGGTTACTGGGTCTCGGTGATTCAGAA 300
    |||||||
Db 241 CTGCGCGTTGATTTCTTGTCTCACCTGGATGAGGTTACTGGGTCTCGGTGATTCAGAA 300
QY 301 TACACCTACTTTTGCATGAGGAGAGATTAATGATTAACAGACTTCAAGACTTTGAGACC 360
    |||||||
Db 301 TACACCTACTTTTGCATGAGGAGAGATTAATGATTAACAGACTTCAAGACTTTGAGACC 360
QY 361 CGGATTTCTATGACACTGACATGACATGACATGATGATGATGATGATGATGATGATGAT 420
    |||||||
Db 361 CGGATTTCTATGACACTGACATGACATGACATGATGATGATGATGATGATGATGATGAT 420
QY 421 CCGTGATTTGTGACTCTGTGCGCAGCCCTCGAAGAGCAATTTAGTCAAGCAGAGACAA 480
    |||||||
Db 421 CCGTGATTTGTGACTCTGTGCGCAGCCCTCGAAGAGCAATTTAGTCAAGCAGAGACAA 480
QY 481 GAGAGATTAAGTGGCGCACTCCGCGGTGATCAGCTGATCTGTGAGGACAGACCTGTG 540
    |||||||
Db 481 GAGAGATTAAGTGGCGCACTCCGCGGTGATCAGCTGATCTGTGAGGACAGACCTGTG 540
QY 541 AAGTCAGAGCTGTACACATTAATTCATGACAGCTTCTGAGATTCGATGATTCAGGA 600
    |||||||
Db 541 AAGTCAGAGCTGTACACATTAATTCATGACAGCTTCTGAGATTCGATGATTCAGGA 600
QY 601 AGAAAGATTTCTGAGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCAATGTTGTA 660
    |||||||
Db 601 AGAAAGATTTCTGAGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCAATGTTGTA 660
QY 661 ATGAGAGCTTTGAGTCTCTACCTACCGGTGGGTACCCACCTCTCAACAAAGCCTCTCTG 720
    |||||||
Db 661 ATGAGAGCTTTGAGTCTCTACCTACCGGTGGGTACCCACCTCTCAACAAAGCCTCTCTG 720
QY 721 AATATTCCTGTTTACCCCGAGATATTTACAGTATCATCTGACAGAGTCTCTTGGCAG 780
    |||||||
Db 721 AATATTCCTGTTTACCCCGAGATATTTACAGTATCATCTGACAGAGTCTCTTGGCAG 780
QY 781 GAGGAAGCCCAAGATCTGTGACTTACAGACATCCAGTTTTCAGAGTCCCAATTTCAAG 840
    |||||||
Db 781 GAGGAAGCCCAAGATCTGTGACTTACAGACATCCAGTTTTCAGAGTCCCAATTTCAAG 840
QY 841 GCAATTAACCTTACTACGATGATGCATTAACCAACCACTGCTGCTGATGATTTGACAT 900
    |||||||
Db 841 GCAATTAACCTTACTACGATGATGCATTAACCAACCACTGCTGCTGATGATTTGACAT 900
QY 901 TCAATACAGACTTTTCTATACAGCTGAGAGATCTTACGCGGATCTGCGCTAACAGT 960
    |||||||
Db 901 TCAATACAGACTTTTCTATACAGCTGAGAGATCTTACGCGGATCTGCGCTAACAGT 960
QY 961 GATTCTGAGGTACAAAGCTTACTCAAAAGACTGACGCTTGAAGATTAAGAGACACTGCG 1020
    |||||||

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RESULT 5
US-09-371-347-45
: Sequence 45, Application US/09371347
: Publication No. US20030082676A1
: GENERAL INFORMATION:
: APPLICANT: Roy A. Gravel et al.
: TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
: TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
: FILE REFERENCE: 50004/003003
: CURRENT APPLICATION NUMBER: US/09/371,347
: PRIOR APPLICATION NUMBER: 60/071,622
: PRIOR FILING DATE: 1998-01-16
: PRIOR APPLICATION NUMBER: 09/232,028
: PRIOR FILING DATE: 1999-01-15
: NUMBER OF SEQ ID NOS: 51
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 45
: LENGTH: 2094

```

Db	961	GATTCTGAGGTACAAACCCCTACTCTCCAAAGACTGAGCTTGAAAGTAAAGAGACACTGC	1020
OY	1021	GTCCCTTTTGAAAATTAAGGCAGACACAAGAAGAAGAGCTACCTTACCCCAGCATATA	1080
Db	1021	GTCCCTTTTGAAAATTAAGGCAGACACAAGAAGAAGAGCTACCTTACCCCAGCATATA	1080
OY	1081	CCCTGGGGGAGTCTCTCCCACTTATTTTAACTCCGCTCTTGAAATCCGAGCAATTCT	1140
Db	1081	CCCTGGGGGAGTCTCTCCCACTTATTTTAACTCCGCTCTTGAAATCCGAGCAATTCT	1140
OY	1141	AAAAAGCATTTTGTGCAGCCCTGTGGACTATACAGTGACAGTGCCTGAAAACGGCAGG	1200
Db	1141	AAAAAGCATTTTGTGCAGCCCTGTGGACTATACAGTGACAGTGCCTGAAAACGGCAGG	1200
OY	1201	CTACAGAGAGCTGTGACAGTAAACAAGGGGAGCCGATTATAGCCGCTTTGTACGAGATGCC	1260
Db	1201	CTACAGAGAGCTGTGACAGTAAACAAGGGGAGCCGATTATAGCCGCTTTGTACGAGATGCC	1260
OY	1261	TGTGCTGCTGTTGTTGGATCTCTCTCTGCTTTCCCTCTTCCGACCCACACTAGTCTC	1320
Db	1261	TGTGCTGCTGTTGTTGGATCTCTCTCTGCTTTCCCTCTTCCGACCCACACTAGTCTC	1320
OY	1321	CTGCTCGAACACTTCTCCAAACCTCAACCCAGACACATATTCGTCGCAAGCTCAAGTTTA	1380
Db	1321	CTGCTCGAACACTTCTCCAAACCTCAACCCAGACACATATTCGTCGCAAGCTCAAGTTTA	1380
OY	1381	TTTTCCACCAGAAAGCTCCTATTTGTCCTCAACATTTGTGCAATTTCTGTCTACGCCACA	1440
Db	1381	TTTTCCACCAGAAAGCTCCTATTTGTCCTCAACATTTGTGCAATTTCTGTCTACGCCACA	1440
OY	1441	ACAGAGGTTCTGGGGAAAGGAGTATGTACAGGCTGGCTGGCTTGTGGTCTTCAGTT	1500
Db	1441	ACAGAGGTTCTGGGGAAAGGAGTATGTACAGGCTGGCTGGCTTGTGGTCTTCAGTT	1500
OY	1501	CTTACGCAAAACATACATGCAATGCCATGANAACAGCGGGAAGCCCTGGCTCCCTAAGTA	1560
Db	1501	CTTACGCAAAACATACATGCAATGCCATGANAACAGCGGGAAGCCCTGGCTCCCTAAGTA	1560
OY	1561	TCCATCTCTCCCGAACAAACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC	1620
Db	1561	TCCATCTCTCCCGAACAAACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC	1620
OY	1621	ATATATGGTGGTCCAGAACCCGCGATAGCCCGTTTATTTGGTCTCTAACAACATAGAGAG	1680
Db	1621	ATATATGGTGGTCCAGAACCCGCGATAGCCCGTTTATTTGGTCTCTAACAACATAGAGAG	1680
OY	1681	AAACTCCAAAGAACACCCAGATGGAATTTTGGACCAATGTGGTGTTTTTGGCTGC	1740
Db	1681	AAACTCCAAAGAACACCCAGATGGAATTTTGGACCAATGTGGTGTTTTTGGCTGC	1740
OY	1741	AGGCAATAAGATTAAGGATTTATCTATTCAGAAAAGCTCAGACATTTTCCCTTAAGCATGG	1800
Db	1738	AGGCAATAAGATTAAGGATTTATCTATTCAGAAAAGCTCAGACATTTTCCCTTAAGCATGG	1797
OY	1801	ATCTTAACTCATTAAGGTTTCTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAAACC	1860
Db	1798	ATCTTAACTCATTAAGGTTTCTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAAACC	1857
OY	1861	CCACCAAAAGTATGTACAAGACACATCCAGTTATGGCCACAGCGAGTGGCAGAAATCCTC	1920
Db	1858	CCACCAAAAGTATGTACAAGACACATCCAGTTATGGCCACAGCGAGTGGCAGAAATCCTC	1917
OY	1921	CTCCAGAGAAAGGCGCATTTTATGTGTGTGTCGATGCAAAAGATATGCGCCAAAGATGTA	1980
Db	1918	CTCCAGAGAAAGGCGCATTTTATGTGTGTGTCGATGCAAAAGATATGCGCCAAAGATGTA	1977
OY	1981	CATGATGCCCTTGTGCAAAATTAATTAAGCAAAAGAGTTGGAGTTGAAAACCTAAGAGCATG	2040
Db	1978	CATGATGCCCTTGTGCAAAATTAATTAAGCAAAAGAGTTGGAGTTGAAAACCTAAGAGCATG	2037
OY	2041	AAAAACCTGGCCACTTTTAAAAGAAAACGTAACCTTCAGATATTTGGTCATTA 2097	

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Db      2038  AAAACCCGCGACCTTTAAAGAGAGAAAACCGCTACCTTCAGAGATTTGGTCATNAA 2094

RESULT 6
US-09-371-347-47
: Sequence 47, Application US/09371347
: Publication No. US20030082676A1
: GENERAL INFORMATION:
:   APPLICANT: Roy A. Gravel et al.
:   TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
:   TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
:   TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
:   FILE REFERENCE: 50004/003003
:   CURRENT APPLICATION NUMBER: US/09/371,347
:   CURRENT FILING DATE: 1999-08-10
:   PRIOR APPLICATION NUMBER: 60/071,622
:   PRIOR FILING DATE: 1998-01-16
:   PRIOR APPLICATION NUMBER: 09/232,028
:   PRIOR FILING DATE: 1999-01-15
:   NUMBER OF SEQ ID NOS: 51
:   SOFTWARE: FASTSEQ for Windows Version 4.0
:   SEQ ID NO 47
:   LENGTH: 2093
:   TYPE: DNA
:   ORGANISM: Homo sapiens
US-09-371-347-47

Query Match      99.1%; Score 2077.4; DB 12; Length 2093;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2092; Conservative 0; Mismatches 1; Indels 4; Gaps 1

QY      1  ATGAGGAGGTTTCTGTTACTATATGCTCTACAGACAGGAGGACAGCAAGGCCATCGCAGAA 60
DB      1  ATGAGGAGGTTTCTGTTACTATATGCTCTACAGACAGGAGGACAGCAAGGCCATCGCAGAA 60

QY      61  GAATGTGTGACGACGCTGTGTACATGGAATTTTTCGAGATCTTCACTATATTAGTGA 120
DB      61  GAAATGTGTGACGACGCTGTGTACATGGAATTTTTCGAGATCTTCACTATATTAGTGA 120

QY      121  TCCGATAGTATGACCTTAAAAACCAACAGCTCCTTTGTTGTGTGGTTTCTACCAAG 180
DB      121  TCCGATAGTATGACCTTAAAAACCAACAGCTCCTTTGTTGTGTGGTTTCTACCAAG 180

QY      121  TCCGATAGTATGACCTTAAAAACCAACAGCTCCTTTGTTGTGTGGTTTCTACCAAG 180
DB      121  TCCGATAGTATGACCTTAAAAACCAACAGCTCCTTTGTTGTGTGGTTTCTACCAAG 180

QY      181  GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
DB      181  GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240

QY      241  CTGCGGGTTGATTTCTTTGCTCACCCTGGGATATGGGTTACATGGGCTCTGGTGATTCA 300
DB      241  CTGCGGGTTGATTTCTTTGCTCACCCTGGGATATGGGTTACATGGGCTCTGGTGATTCA 300

QY      301  TACACCTACTTTTGGCAATGGGGGGGAAGATTAATGTAAACGACTCAAGAGCTTGGAGCC 360
DB      301  TACACCTACTTTTGGCAATGGGGGGGAAGATTAATGTAAACGACTCAAGAGCTTGGAGCC 360

QY      361  CGGCATTTCTATGACACTGGAATGCAATGCAATGACTGTGATGTTTGAAGCTTGTGGTTG 420
DB      361  CGGCATTTCTATGACACTGGAATGCAATGCAATGACTGTGATGTTTGAAGCTTGTGGTTG 420

QY      421  CCGTGTGATTTGCTGCACTTGGCCAGCCCTCAGAAAGCAATTTTAACTCAAGAGAGACAA 480
DB      421  CCGTGTGATTTGCTGCACTTGGCCAGCCCTCAGAAAGCAATTTTAACTCAAGAGAGACAA 480

QY      481  GAGGAGATTAATGGGCGACCTCCCGGTGGCATACCTGGATCCTTAAAGACAGACCTTGG 540
DB      481  GAGGAGATTAATGGGCGACCTCCCGGTGGCATACCTGGATCCTTAAAGACAGACCTTGG 540

QY      541  AAGTCAGAGCTGCTACATATTGAATCTGAAGTCGACTTCTGAGATTGCGATATTCAAGA 600
DB      541  AAGTCAGAGCTGCTACATATTGAATCTGAAGTCGACTTCTGAGATTGCGATATTCAAGA 600

QY      601  AGAAAGATTCTGAGGTTTGAAGCAAAATGCATGAACAGCAACCAATTCATGTTGTA 660
DB      601  AGAAAGATTCTGAGGTTTGAAGCAAAATGCATGAACAGCAACCAATTCATGTTGTA 660

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Db 601 AGAAGATTCGAGGTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCATGTTGTA 660
Oy 661 ATGAGACTTTGAGTCCCTCACTTACCCTGGGACCCCACTGTCACAGCCCTCTG 720
Db 661 ATGAGACTTTGAGTCCCTCACTTACCCTGGGACCCCACTGTCACAGCCCTCTG 720
Oy 721 AATATTCCTGTTTACCCCGAATATTACAGTACATGCAAGAGTCTTGGCCAG 780
Db 721 AATATTCCTGTTTACCCCGAATATTACAGTACATGCAAGAGTCTTGGCCAG 780
Oy 781 GAGAAAGCCCAAGATCTGTGACTTCAGACATCCAGTTTTCAGAGTCCCAATTTCAAG 840
Db 781 GAGAAAGCCCAAGATCTGTGACTTCAGACATCCAGTTTTCAGAGTCCCAATTTCAAG 840
Oy 841 GCAGTTCACTTACTAGCATGATGCCATTAACCACTGCTGCTGATGATGAGTGGACAT 900
Db 841 GCAGTTCACTTACTAGCATGATGCCATTAACCACTGCTGCTGATGATGAGTGGACAT 900
Oy 901 TCAATACAGACTTTTCTATCAGCTGGAGATGCTTACAGCTGATCTGCCCTAACAT 960
Db 901 TCAATACAGACTTTTCTATCAGCTGGAGATGCTTACAGCTGATCTGCCCTAACAT 960
Oy 961 GATTCGAGTACAAAGCTCTCTCCAAAGACTGCAGCTTGAAGATAAAGAGACATGC 1020
Db 961 GATTCGAGTACAAAGCTCTCTCCAAAGACTGCAGCTTGAAGATAAAGAGACATGC 1020
Oy 1021 GTCCCTTTGAATAAAGCGACACAAGAAAGAGAGCTTACCTCCAGCATATA 1080
Db 1021 GTCCCTTTGAATAAAGCGACACAAGAAAGAGAGCTTACCTCCAGCATATA 1080
Oy 1081 CCTCGGGAGTCTCTCCAGTCAATTTTACCTGCTGCTTGAATTCGAGCAATTCCT 1140
Db 1081 CCTCGGGAGTCTCTCCAGTCAATTTTACCTGCTGCTTGAATTCGAGCAATTCCT 1140
Oy 1141 AAAAGGATTTTGGCGCCCTGTGACTATACAGTGACAGTGGAGAAAGCGCAGG 1200
Db 1141 AAAAGGATTTTGGCGCCCTGTGACTATACAGTGACAGTGGAGAAAGCGCAGG 1200
Oy 1201 CTACAGAGCTGTGCACTAAACAAGGGGACCGCATTAATAGCCCTTTGTACGAGATGCC 1260
Db 1201 CTACAGAGCTGTGCACTAAACAAGGGGACCGCATTAATAGCCCTTTGTACGAGATGCC 1260
Oy 1261 TGTGCTGCTGTTGGATCTCTCTGCTTCCCTTCTGCGACACACTGAGTCTC 1320
Db 1261 TGTGCTGCTGTTGGATCTCTCTGCTTCCCTTCTGCGACACACTGAGTCTC 1320
Oy 1321 CTGCTCGACATCTTCTAACTCAACCCAGACCATATTCGTGCAAGCTCAAGTTA 1380
Db 1321 CTGCTCGACATCTTCTAACTCAACCCAGACCATATTCGTGCAAGCTCAAGTTA 1380
Oy 1381 TTTACCCAGGAAAGCTCATTTTGTCTTCAACATTGTGAATTGTGTCTACGCCACA 1440
Db 1381 TTTACCCAGGAAAGCTCATTTTGTCTTCAACATTGTGAATTGTGTCTACGCCACA 1440
Oy 1441 ACAGAGTTCGCGGAAGGAGTATGTACAGGCTGGCTGCTGTTGGTTCCTCAGTT 1500
Db 1441 ACAGAGTTCGCGGAAGGAGTATGTACAGGCTGGCTGCTGTTGGTTCCTCAGTT 1500
Oy 1501 CTTGAGCCAAACATACATGATCCCATGAAGACAGCGGAAAGCCCTGCTCCCAAGTA 1560
Db 1501 CTTGAGCCAAACATACATGATCCCATGAAGACAGCGGAAAGCCCTGCTCCCAAGTA 1560
Oy 1561 TCCATCTCTCTCGAACAACAAATTTTCCACTTACAGATGACCCCTCAATCCCATC 1620
Db 1561 TCCATCTCTCTCGAACAACAAATTTTCCACTTACAGATGACCCCTCAATCCCATC 1620
Oy 1621 ATATATGTTGGTCCAGAACCGGATAGCCCTTATGTTGGTCTCAACAACAT ---AG 1676
Db 1621 ATATATGTTGGTCCAGAACCGGATAGCCCTTATGTTGGTCTCAACAACAT ---AG 1676
Oy 1681 AAATCCAGAACACACCCAGATGAAATTTTGGACATATGTTGGTCTGCTGC 1740
Db 1681 AAATCCAGAACACACCCAGATGAAATTTTGGACATATGTTGGTCTGCTGC 1740
Oy 1677 AAATCCAGAACACACCCAGATGAAATTTTGGACATATGTTGGTCTGCTGC 1736

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Oy 1741 AGCATAGAGATFAGGATTATCTATTCAGAAAGAGCTCAGACATTTCTTACATGGG 1800
Db 1737 AGCATAGAGATFAGGATTATCTATTCAGAAAGAGCTCAGACATTTCTTACATGGG 1736
Oy 1801 ATCTTAATCATCTAAAGGTTTCTTCAAGAGATGCTCTGTTGGGAGAGAAAGCC 1860
Db 1797 ATCTTAATCATCTAAAGGTTTCTTCAAGAGATGCTCTGTTGGGAGAGAAAGCC 1856
Oy 1861 CCAGCAAGTATGTACAAAGAACATTCAGCTTATGAGCCAGCAGGTTGGCAGATCTC 1920
Db 1857 CCAGCAAGTATGTACAAAGAACATTCAGCTTATGAGCCAGCAGGTTGGCAGATCTC 1916
Oy 1921 CTCCAGAGAGAGGCGCATTTATGTGTGTGAGATGCAAGATATGAGGCAAGATGTA 1980
Db 1917 CTCCAGAGAGAGGCGCATTTATGTGTGTGAGATGCAAGATATGAGGCAAGATGTA 1976
Oy 1981 CATGATGCCCTTGTGCAATATATAAGCAAGAGGTTGAGTTGAAAACATAAGACATG 2040
Db 1977 CATGATGCCCTTGTGCAATATATAAGCAAGAGGTTGAGTTGAAAACATAAGACATG 2036
Oy 2041 AAAACCTGGCCACTTTAAAGAAAGAAACCGTACCTTACAGATATTGGTCAATA 2097
Db 2037 AAAACCTGGCCACTTTAAAGAAAGAAACCGTACCTTACAGATATTGGTCAATA 2093

RESULT 7
US-09-567B-38
; Sequence 38, Application US/0909567B
; Publication No. US20030022257A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto A.
; APPLICANT: Nair, Manoj
; APPLICANT: Chen, Selju
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
; FILE REFERENCE: DEX-0214
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,834
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 2475
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1001)..(1011)
; OTHER INFORMATION: a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1011)..(1011)
; OTHER INFORMATION: a, c, g or t
US-09-909-567B-38

Query Match 8.3%; Score 174.4; DB 12; Length 2475;
Best Local Similarity 96.7%; Pred. No. 1.1e-44;
Matches 178; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 510 ATCACTGCATCTCTGAGAGACGACCTTGTGAAGTCAAGAGCTGTACACATTAAGTCA 569
Db 1 ATCACTGCATCTCTGAGAGACGACGACCTTGTGAAGTCAAGAGCTGTACACATTAAGTCA 60
Oy 570 AGTGAGCTTGTGAGATTCGATGTTCAGAGAAAGAGATTTGAGTTTGAAGCAAA 629
Db 61 AGTGAGCTTGTGAGATTCGATGTTCAGAGAAAGAGATTTGAGTTTGAAGCAAA 120
Oy 630 TGCAGTGAACGCAACCAATCCATGTTGTAATGAAGACTTGAAGTCCATACCTACCG 689
Db 121 TGCAGTGAACGCAACCAATCCATGTTGTAATGAAGACTTGAAGTCCATACCTACCG 180
Oy 690 TTCG 693

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QY 1888 CAGCTTCATGCGCCAGGATGCGAGAACTCTCTCCAGAGAGAGCCCATATTATG 1947
DB 1832 AAGAGAGACAGGAGAACCTGTGGAGCTGATCCAGAGGGGGTCCCATCTATGTG 1891
QY 1948 TGTGAGATGCAAGATATGTGGCCCAAGATGTACA 1982
DB 1892 TCGGGGATGCTCGAAATATGCGCAAGATGTGCA 1926

RESULT 10
US-09-783-590-1364
Sequence 1364, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haselbine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16, 2C1
CURRENT APPLICATION NUMBER: US/09/783,590
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1364
LENGTH: 101
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (2)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (62)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-1364

Query Match
Best Local Similarity 95.0%; Score 83.8; DB 11; Length 101;
Matches 96; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1673 ATAGGAGAACTCCAGACACACCCAGATGGAATTTGGAGCAATGTGTTGTTT 1732
DB 1 ANAGAGAGAACTCCAGACACACCCAGATGGAATTTGGAGCAATGTGTTGTTT 60
QY 1733 TGGCTGCAGCATAGATAGG-ATTATCATTCAGAAA 1772
DB 61 TNGCTGCAGCATAGATAGGTTAGGCAATTATCTATTCAGAAA 101

RESULT 11
US-09-294-093B-4842
Sequence 4842, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:
APPLICANT: Laljudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL Program
SEQ ID NO 4842

LENGTH: 298
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700355168H1
US-09-294-093B-4842

Query Match
Best Local Similarity 58.0%; Score 61; DB 10; Length 298;
Matches 148; Conservative 0; Mismatches 100; Indels 7; Gaps 2;

QY 1587 TTTCACCTACAGATGACCCCTCAATCCCATCATATGATGGTCCAGAACCGGAT 1646
DB 46 TTTCAGATGCTGATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 104
QY 1647 AGCCCGTTTATTTGGTTCTTCAACATATGAGAGAACTCCAGAACACCCAGATG 1706
DB 105 GGCTCCTTTAGAGGTTCTTTCAGAGAAAGTTAGCACTGAAACAAAT-----CTGAGC 158
QY 1707 AAATTTGAGCATATGTGTTGTTTGGCTGCGAGCATATAGGATATATCTTT 1766
DB 159 AGAAGTGGGCACTTCAATCTTTCTTTGGATGAGAGAACCGTAATATGACTACATATA 218
QY 1767 CAGAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCTATTAAGTTCTT 1826
DB 219 TGAAGATAGCTGCAAACTTTCTTCTTGGATGAGAGAGGGGCGCTTCTGAGCTAATTTGTCATT 278
QY 1827 CTCAGAGATGCTCC 1841
DB 279 CTCGCGGAGAGGGCC 293

RESULT 12
US-09-822-849A-278
Sequence 278, Application US/09822849A
Patent No. US20020045170A1
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakari
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 278
LENGTH: 2470
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-849A-278

Query Match
Best Local Similarity 55.6%; Score 59.6; DB 10; Length 2470;
Matches 138; Conservative 0; Mismatches 104; Indels 6; Gaps 1;

QY 1588 TTTCACCTACAGATGACCCCTCAATCCCATCATATGATGGTCCAGAACCGGAT 1647
DB 1615 TTTCAGCTGCTTCAAGCCACACACCGCTTCTATCATATGATGGGCGGCGGAGTG 1674
QY 1648 GCGCCGTTATTTGGTTCTTCAACATATGAGAGAACTCCAGAACACCCAGATGGA 1707
DB 1675 GCACCTTCATATGAGGCTTCAATCCAGAGGCGCTGGCTGCGAGCAGGAGAGG-- 1732

US-09-938-842A-803
 RESULT 15
 Sequence 803 Application US/09938842A
 Patent No. US20020160378A1
 GENERAL INFORMATION:
 APPLICANT: Harper, Jeff
 APPLICANT: Kreps, Joel
 APPLICANT: Wang, Xun
 APPLICANT: Zhu, Tong
 TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 TITLE OF INVENTION: SAME, AND METHODS OF USE
 FILE REFERENCE: SCRIPT300-3
 CURRENT APPLICATION NUMBER: US/09/938,842A
 CURRENT FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: US 60/227,886
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: US 60/264,647
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/300,111
 PRIOR FILING DATE: 2001-06-22
 NUMBER OF SEQ ID NOS: 5379
 SEQ ID NO 803
 LENGTH: 2136
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-09-938-842A-803

Query Match	2.78;	Score 56;	DB 11;	Length 2136;
Best Local Similarity	54.38;	Pred. No. 1.6e-06;		
Matches 138;	Conservative 0;	Mismatches 110;	Indels 6;	Gaps 1;

OY	1588	TTCCACCTTACCAGATGAGACCCCATCCCAATCATAATGGGTGCCAGAACCGGCATA	164
Db	1657	TTCAAAGCTTCCTTGATTCTTAAGTACCGAATCATGATCGGCCAGGGACTGGATTA	1718
OY	1648	GCCCCGTTTATTTGGTTCCTCAACAATGAGAGAACTCCAAGAACAACCCACAGATGA	1707
Db	1717	GCTCCATTCACAGAGATTCCTTCACAGAAAGACTAGCGTTGGTAGAAT-----CTGGTITT	1770
OY	1708	AATTTGGAGCAATGTSGTGTCTTTTTTGGCTGCAGGCATTAAGATAGGCAATTAATCTATTC	1767
Db	1771	GAACTTGGGCGCATCAGTTTGTCTTTTGGATGACGAAAACCCGTAGAAATGATTTCACTCAC	1830
OY	1768	AGAAAGAGAGCTACAGACATTTCTTAAAGCATGGAGATCTTAACATCACTTAAAGTTTCCCTTC	1827
Db	1831	GAGGAGAGAGCTCCACGCGATTTGTGGAGAGTGTGCTCTCGCAGACCTTAAGTGTGCGCTTC	1890
OY	1828	TCAAGAGATGCTCC	1841
Db	1891	TTCTGCTGAAGGACC	1904

Search completed: July 29, 2003, 23:03:18
Job time : 427.084 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2003, 09:58:39 ; Search time 89.0595 Seconds
(without alignments)
7221.032 Million cell updates/sec

Title: US-09-371-347A-43

Perfect score: 2097

Sequence: 1 atgaggaggttcgtctact.....ttcagatattgtcataa 2097

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued_Patents_NA.*
- 2: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCtUS.COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2095.4	99.9	3259	4	US-09-318-448-23
2	386.4	18.4	390	4	US-08-905-223-71
3	63.6	3.0	4353	2	US-08-365-486A-18
4	63.6	3.0	4353	4	US-08-880-342-18
5	63.6	3.0	4780	2	US-08-365-486A-20
6	63.6	3.0	4780	3	US-09-123-708-3
7	63.6	3.0	4780	3	US-09-123-708-3
8	63.6	3.0	4780	4	US-08-880-342-20
9	57.2	2.7	5057	2	US-08-365-486A-12
10	57.2	2.7	5057	4	US-08-880-342-12
11	57.2	2.7	5108	1	US-07-642-002-1
12	53.6	2.6	1863	4	US-09-627-216A-13
13	53.6	2.6	1890	4	US-09-134-001C-1557
14	50.2	2.4	1448	4	US-08-936-165A-113
15	49.2	2.3	4145	4	US-09-302-620B-82
16	46.2	2.2	7218	1	US-08-232-463-14
17	46.2	2.2	4206	4	US-09-303-620B-81
18	44.4	2.1	307	4	US-09-172-711-24
19	43.4	2.1	7218	1	US-08-232-463-14
20	40.6	1.9	382	4	US-08-976-259-78
21	39.6	1.9	4041	1	US-08-147-812-4
22	39.6	1.9	4110	3	US-09-123-708-1
23	39.6	1.9	4110	3	US-09-123-708-1
24	39.6	1.9	4165	1	US-08-147-812-6
25	36.6	1.7	3701	1	US-08-553-279-1
26	36.6	1.7	45546	4	US-09-146-053-6
27	36	1.7	4089	1	US-07-908-245-1

28	36	1.7	4097	3	US-09-123-708-5	Sequence 5, Appl1
29	36	1.7	4097	3	US-09-123-708-5	Sequence 5, Appl1
30	35.4	1.7	1296	4	US-09-134-001C-1501	Sequence 1501, Ap
31	34.2	1.6	1569	1	US-08-680-726A-57	Sequence 57, Appl
32	34.2	1.6	1569	3	US-09-092-409-57	Sequence 57, Appl
33	34.2	1.6	10592	1	US-08-680-726A-51	Sequence 51, Appl
34	34.2	1.6	10592	1	US-08-680-726A-52	Sequence 52, Appl
35	34.2	1.6	10592	3	US-09-092-409-51	Sequence 51, Appl
36	34.2	1.6	10592	3	US-09-092-409-52	Sequence 52, Appl
37	34	1.6	2223	1	US-08-257-073-4	Sequence 4, Appl1
38	33.8	1.6	1702	1	US-08-261-822A-14	Sequence 14, Appl
39	33.8	1.6	1702	5	PCT-US95-07744A-14	Sequence 14, Appl
40	33.8	1.6	4146	1	US-08-261-822A-15	Sequence 15, Appl
41	33.8	1.6	4146	5	PCT-US95-07744A-15	Sequence 15, Appl
42	33.2	1.6	2277	1	US-08-676-967-2	Sequence 2, Appl1
43	33.2	1.6	2277	1	US-08-676-974-2	Sequence 2, Appl1
44	33.2	1.6	2277	2	US-09-098-487-2	Sequence 2, Appl1
45	32.6	1.6	2193	4	US-09-427-261-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1									
US-09-318-448-23									
Sequence 23, Application US/09318448									
Patent No. 6210950									
GENERAL INFORMATION:									
APPLICANT: Johnson, William G.									
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING									
FILE REFERENCE: 601-1-057									
CURRENT FILING DATE: 1999-05-25									
NUMBER OF SEQ ID NOS: 46									
SOFTWARE: Patentlin Ver. 2.0									
SEQ ID NO 23									
LENGTH: 3259									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-09-318-448-23									
Query Match									
Best Local Similarity 99.9% Score 2095.4; DB 4; Length 3259;									
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	1	ATGAGAGAGTTTCTGTACTATATGCTACACAGCAGGAGCAAGGCCATCGCAGAA	60						
DB	80	ATGAGAGAGTTTCTGTACTATATGCTACACAGCAGGAGCAAGGCCATCGCAGAA	139						
QY	61	GAATGTGTGAGCAAGCTGTGTACATGATTTTTCAGAGATCTTCACTATATTAGTGA	120						
DB	140	GAATGTGTGAGCAAGCTGTGTACATGATTTTTCAGAGATCTTCACTATATTAGTGA	199						
QY	121	TCCGTAAGTATGACTTAAACCAACAGCTCTCTGTGTGTGTGTGTCTTACACAG	180						
DB	200	TCCGTAAGTATGACTTAAACCAACAGCTCTCTGTGTGTGTGTGTCTTACACAG	259						
QY	181	GGCAGCGAGAGCCACCCGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCAAA	240						
DB	260	GGCAGCGAGAGCCACCCGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCAAA	319						
QY	241	CTGCCGTTGATTTTCTGCTACCTGCGGTATGGGTTACTGCTGCTGCTGCTGCTG	300						
DB	320	CTGCCGTTGATTTTCTGCTACCTGCGGTATGGGTTACTGCTGCTGCTGCTGCTG	379						
QY	301	TACACCTACTTTTGAATGGGGGAAGATTAATGAATGAATGAATGAATGAATGAAT	360						
DB	380	TACACCTACTTTTGAATGGGGGAAGATTAATGAATGAATGAATGAATGAATGAAT	439						
QY	361	CGGCAATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGAC	420						

440 CGGATTTCTATGACACTGACATGACATGACTGTAGGTTAGAACTTGTTGGTAG 499
421 CCGTGGATTTGGTGAAGCTGTGGCCAGCCCTCAGAAAGCATTTTAGTCAAGCAGAGACAA 480
500 CCGTGGATTTGGTGAAGCTGTGGCCAGCCCTCAGAAAGCATTTTAGTCAAGCAGAGACAA 559
481 GAGCAGATTAAGTGGCGCACTCCCGGTGACATCAGCTGCAATCCCTTGAGACAGACCTGTG 540
560 GAGGAGATTAAGTGGCGCACTCCCGGTGACATCAGCTGCAATCCCTTGAGACAGACCTGTG 619
541 AAGTCAGAGCTGCTCAGATGAATCTCAGTCGAGCTTGAGATTTGGATGATGATCAGA 600
620 AAGTCAGAGCTGCTCAGATGAATCTCAGTCGAGCTTGAGATTTGGATGATGATCAGA 679
601 AGAAAGATTTGAGGTTTGAAGCAAAATGAGTGAAGCAGACCAATCCCAATGTTGTA 660
680 AGAAAGATTTGAGGTTTGAAGCAAAATGAGTGAAGCAGACCAATCCCAATGTTGTA 739
661 ATTGAAGCTTTGAGTCTCTCAGCTTACCCGTTGCGTACCCCACTCTCAAGCCCTCTGTG 720
740 ATTGAAGCTTTGAGTCTCTCAGCTTACCCGTTGCGTACCCCACTCTCAAGCCCTCTGTG 799
721 AATATTCCTGTTTACCCCAAGATTTTACAGTACATCTGACAGAGATCTCTTGGCCAG 780
800 AATATTCCTGTTTACCCCAAGATTTTACAGTACATCTGACAGAGATCTCTTGGCCAG 859
781 GAGCAAGCCCAAGATTTTGTGACTTACAGTACATCTGAGTTCAGAGTCCCAATTTCAAG 840
860 GAGCAAGCCCAAGATTTTGTGACTTACAGTACATCTGAGTTCAGAGTCCCAATTTCAAG 919
841 GCAGTCACTTACAGTACATCTGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGT 900
920 GCAGTCACTTACAGTACATCTGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGT 979
901 TCAATATCAGACTTTTCTATCAGCTGAGATGCTTACAGTTCAGAGTTCAGAGTTCAGAGT 960
980 TCAATATCAGACTTTTCTATCAGCTGAGATGCTTACAGTTCAGAGTTCAGAGTTCAGAGT 1039
961 GATTCGAGTACAAAGCTTCTCAAGACTGACGCTTGAAGATTAAGAGAGAGAGAGAGAGAG 1020
1040 GATTCGAGTACAAAGCTTCTCAAGACTGACGCTTGAAGATTAAGAGAGAGAGAGAGAGAG 1099
1021 GTCCCTTTGAAATTAAGGACGACACAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1100 GTCCCTTTGAAATTAAGGACGACACAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1159
1081 CCTGCGGAGTGTCTCTCAGTCAATTTTACCTGCTCTTGAATCCGAGCAATTTCT 1140
1160 CCTGCGGAGTGTCTCTCAGTCAATTTTACCTGCTCTTGAATCCGAGCAATTTCT 1219
1141 AAAAAGCATTTTGGCAGCCCTTGTGAGTATACAGTGAAGTGAAGAGAGAGAGAGAGAG 1200
1220 AAAAAGCATTTTGGCAGCCCTTGTGAGTATACAGTGAAGTGAAGAGAGAGAGAGAGAG 1279
1201 CTACAGAGAGTGTGAGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
1280 CTACAGAGAGTGTGAGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1339
1261 TGTGCTGCTGTTGAGATCTCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
1340 TGTGCTGCTGTTGAGATCTCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1399
1321 CTGCTCGAATCT 1380
1400 CTGCTCGAATCT 1459
1381 TTTACCCAG 1440
1460 TTTACCCAG 1519
1441 ACAGAGGTTCTGCGAAGAGAGAGATGTACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1500
1520 ACAGAGGTTCTGCGAAGAGAGAGATGTACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1579

1501 CTTACGCCAAACATATCATGATCCCATGAGACAGCGGAGAAAGCCCTGCTCTAAGATA 1560
1580 CTTACGCCAAACATATCATGATCCCATGAGACAGCGGAGAAAGCCCTGCTCTAAGATA 1639
1561 TCCATCTCTCTCTGCAACAACAATTTCTTCCACTTTACAGATGAGACCCCTCAATCCCATC 1620
1640 TCCATCTCTCTCTGCAACAACAATTTCTTCCACTTTACAGATGAGACCCCTCAATCCCATC 1699
1621 AATAAGGAGTCCGAGAACCGGATACCCCGTTATTTGGGTTCTTCAACATAGAGAG 1680
1700 AATAAGGAGTCCGAGAACCGGATACCCCGTTATTTGGGTTCTTCAACATAGAGAG 1759
1681 AAATCTCAAGAACCAACACCCAGATGGAATTTTGGAGCAATGTGTTTGGCTGC 1740
1760 AAATCTCAAGAACCAACACCCAGATGGAATTTTGGAGCAATGTGTTTGGCTGC 1819
1741 AGCATTAAGATAGGATTTATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGG 1800
1820 AGCATTAAGATAGGATTTATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGG 1879
1801 ATCTTAATCATCTTAAGGTTTCTCTCTCAAGATGCTCTGTTGGGAGAGAGAGAGCC 1860
1880 ATCTTAATCATCTTAAGGTTTCTCTCTCAAGATGCTCTGTTGGGAGAGAGAGAGCC 1939
1861 CCAGCAAGATATGTACAGACACATCCAGCTTCATGSCAGAGAGTGGCAGAGATCCTC 1920
1940 CCAGCAAGATATGTACAGACACATCCAGCTTCATGSCAGAGAGTGGCAGAGATCCTC 1999
1921 CTCCAGAGAAAGCCCATATTTATGTGTGAGATGCAAGATATGAGCCAGAGATGA 1980
2000 CTCCAGAGAAAGCCCATATTTATGTGTGAGATGCAAGATATGAGCCAGAGATGA 2059
1981 CATGATGCCCTTGTGCAATATTAAGCAAGAGGTTGAGTGAAGAACTGAAGCATG 2040
2060 CATGATGCCCTTGTGCAATATTAAGCAAGAGGTTGAGTGAAGAACTGAAGCATG 2119
2041 AAAACCCCTGCGCACTTTTAAAGAGAAAGAGCTTACCTTCAGATATTTGGTCTATA 2097
2120 AAAACCCCTGCGCACTTTTAAAGAGAAAGAGCTTACCTTCAGATATTTGGTCTATA 2176

RESULT 2
US-08-905-223-71
Sequence 71, Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelien, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: DOUBLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo Sapiens
 TISSUE TYPE: Brain
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 289..357
 IDENTIFICATION METHOD: Von Heijne matrix
 OTHER INFORMATION: score 6.9
 OTHER INFORMATION: seq SLSLASHSVSC/SN
 US-08-905-223-71

Query Match 18.4%; Score 386.4; DB 4; Length 390;
 Best Local Similarity 99.7%; Pred. No. 2.5e-116;
 Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 968 AGGTACAAAGCCTACTCTCAAGAGCTGACCTTGAAGATAAAGAGACAGCTGCTCTTT 1027
 1 AAGTACAAAGCCTACTCTCAAGAGCTGACCTTGAAGATAAAGAGAGCACTGCTCTTT 60
 QY 1028 TGAATAAAGCAGACACAGCAAGAGAGACTACCTTACCCAGCATATACCTGCGG 1087
 61 TGAATAAAGCAGACACAGCAAGAGAGAGACTACCTTACCCAGCATATACCTGCGG 120
 QY 1088 GATGTTCTCTCAGTTCATTTTACCTGCTGCTTGAATTCGAGCAATTCCTAAAGAG 1147
 121 GATGTTCTCTCAGTTCATTTTACCTGCTGCTTGAATTCGAGCAATTCCTAAAGAG 180
 QY 1148 CATTTTGGAGCCCTTGTGACTATACAGTACAGTCTGTAAGAGCCAGGCTACAGG 1207
 181 CATTTTGGAGCCCTTGTGACTATACAGTACAGTCTGTAAGAGCCAGGCTACAGG 240
 QY 1208 ACTGTGCGATTAACAAGGGGAGCCGATTATAGCCGCTTTGTACAGATGCTGTGCT 1267
 241 ACTGTGCGATTAACAAGGGGAGCCGATTATAGCCGCTTTGTACAGATGCTGTGCT 300
 QY 1268 GCTTGTGATCTCCCTCGCTTCCCTTCTTGGCAGCAGCAGCATCTCTCTGCTG 1327
 301 GCTTGTGATCTCCCTCGCTTCCCTTCTTGGCAGCAGCAGCATCTCTCTGCTG 360
 QY 1328 AACATCTCTCTTAACCTTCAACCCAGAGC 1355
 361 AACATCTCTCTTAACCTTCAACCCAGAGC 388
 Db

RESULT 3

US-08-365-486A-18
 Sequence 18, Application US/08365486A
 Patent No. 5834306
 GENERAL INFORMATION:
 APPLICANT: Webster, Keith A.
 APPLICANT: Bishopric, Nanette H.
 TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESS: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/365,486A
 FILING DATE: 23-DEC-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4353 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 AMTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al,
 INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..4305
 US-08-365-486A-18

Query Match 3.0%; Score 63.6; DB 2; Length 4353;
 Best Local Similarity 48.8%; Pred. No. 5.7e-10;
 Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

QY 1588 TTCCACTTACCAAGATGACCCCTCAATCCCATATATAGTGCGTCCAGAACCGCAT 1647
 3715 TTCCACTTACCAAGATGACCCCTCAATCCCATATATAGTGCGTCCAGAACCGCAT 3774
 QY 1648 GCCCGCTTATGCTGCTTCTACACATPAGAGAACTCCAGAACACCCAGATGGA 1707
 3775 GCCCGCTTATGCTGCTTCTACACATPAGAGAACTCCAGAACACCCAGATGGA 3831
 Db
 QY 1708 AATTTGAGCAATGTGTTGTTTGGCTGAGCATPAGGATPAGGATTAATCTATTC 1767
 3832 AATTTGAGCAATGTGTTGTTTGGCTGAGCATPAGGATPAGGATTAATCTATTC 3891
 QY 1768 AGAAGAGCTCAGACATTTCTTAAGCATGGATCTTAACCTTAAGGTTTCCTTC 1827
 3892 AGAAGAGCTCAGACATTTCTTAAGCATGGATCTTAACCTTAAGGTTTCCTTC 3951
 QY 1828 TCAGAGATGCTCTTGTGGGAGGAGAAAGCCCGCAAGAGATGTACAGACATC 1887
 3952 TCCC-----GGAGCCAGCAAAACCAAGAGATGTACAGACATC 3996
 Db
 QY 1888 CAGCTTCATGGCCAGCAGGTGCGGAGATCTCTCCAGAGAACCGCATATTTATGTG 1947
 3997 CAGCTTCATGGCCAGCAGGTGCGGAGATCTCTCCAGAGAACCGCATATTTATGTG 4056
 QY 1948 GTGTGAGATGCAAGATATGCGCAAGATGTATCATGATGCGCTTGTGCAATATTAAC 2007
 4057 GTGTGAGATGCAAGATATGCGCAAGATGTATCATGATGCGCTTGTGCAATATTAAC 4116
 QY 2008 AAGAGGTTGAGATGTAAGAACTAAGAGCAATGAAGAACTGCGCATTTAAGAGAA 2067
 4117 CAGCAGGGAGAGCTTCGCGAGAGAGCGCGGCGTATTATCAGCCGATGAGGATGAC 4176
 Db
 QY 2068 AAGCGTACCTTCAGATATTT 2089
 4177 AAGCGTACCTTCAGATATTT 4198
 Db

RESULT 4

US-08-880-342-18

Sequence 18, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4353 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al,
J. Neurochem 63:140 1994
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4305
US-08-880-342-18

Query Match 3.0%; Score 63.6; DB 4; Length 4353;
Best Local Similarity 48.8%; Pred. No. 5,7e-10;
Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

QY 1588 TTCGACTTACGATGACGCCCATATCCCATCATATATGTTGGTCCAGAACCGGCATA 1647
DB 3775 TTCGACTTCCCGGACCCGACCAAGTCCCTGATCTGTGGACACAGGCACGGCATTT 3774
QY 1648 GCCCGTTATGTTGCTTCAACATAGAGAGAAGAACACCAACACCAACATGGA 1707
DB 3775 GCCCTTTCCGAAGCTTCTGCAACAGCG---GCAATTTGATATCCACACAAAGGAATG 3831
QY 1708 AATTTTGAGCAATGTGTTGTTTGGCTGACGATTAAGATAGGATATATCTATTC 1767
DB 3832 AACCCCTGCCCATGTCTCTGTTCTCGGGTCCGCGCAATCAACATATATATCTAC 3891

QY 1768 AGAAGAGCTCAGACATTTCTTAAGCATGGCATCTTAATCATCTAAAGTTTCTTC 1827
DB 3892 AGGAAGAGACCTCGAGGCCCAAGACAGGGGTCTTGAGAGAGCTGACAGGCTTAC 3951
QY 1828 TCAAGATGCTCTCTGTTGGGAGAGGAAGCCCAAGCAAGATATGTACAGACAAATC 1887
DB 3952 TCCC-----GGGAGCCAGACAAACCAAGAAAGTACGTGCGAGCATCTCG 3996
QY 1888 CAGCTTCATGGCCAGCAGGTGGGAGAGATCTCTCCAGAGAGAGGCCATATTATTG 1947
DB 3997 CAGGAGCAGCTGGCGGAGATGTGTGTACCGAGCCCTTAAGAGAGAGGGGCCCATATAC 4056
QY 1948 TGTGAGATGCAAGATATGCGCAAGATGTATCATGATGCCCTTGTGCAAAATATAC 2007
DB 4057 GTCTGTGGGAGCGTCAACATGCTGCTGATGTCTCAAAAGCCATCCAGCGCATATGACC 4116
QY 2008 AAGAGTTGCAATGTAAGAACTAAGAAAGCAATAAACCTGGCCACTTTAAAGAGAA 2067
DB 4117 CAGCAGGGGAGAGCTTCGCGCAGAGACGCCGCGTATTATCATGACCGGATGAGAGATAC 4176
QY 2068 AACGCTACCTTCAGATATTT 2089
DB 4177 AACCATACCATAGGATATTT 4198

RESULT 5
US-08-365-486a-20
Sequence 20, Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 4780 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human NOS-3N gene, Nakane, et al,
FEBS Lett 316:175 (1993)
FEATURE:
NAME/KEY: CDS
LOCATION: 431..4732

US-08-365-486A-20

Query Match 3.0%; Score 63.6; DB 2; Length 4780;

Best Local Similarity 48.8%; Pred. No. 6.1e-10;

Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

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Oy 1588 TTCACCTTACAGATGACCCCTCAATCCCATCATATGATGGGTCCAGAAACCGGCATTA 1647
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4142 TTCACCTTACAGATGACCCCTCAATCCCATCATATGATGGGTCCAGAAACCGGCATTA 4201
Oy 1648 GCCCGGTTATTTGGTTCCTCAACATAGAGAAATCCCAAGAACACACCCAGATGGA 1707
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4202 GCCCGGTTATTTGGTTCCTCAACATAGAGAAATCCCAAGAACACACCCAGATGGA 4258
Oy 1708 AATTTTGAGCAATGTGTTGTTTGGCTGACAGGCAATAGATAGGATTAATCTATTC 1767
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4259 AACCCTTCCCATGCTCTGCTGCTTGGGTGCGGCAATCCAGATAGATCATATCTAC 4318
Oy 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGAGATCTTAAGTCAATCAAGGTTTCCTTC 1827
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4319 AGGAGAGAGACCTTCAGAGCCAGAGAACAGGGGGTCTTACAGAGACTGTACACGGCTTAC 4378
Oy 1828 TCAGAGATGCTCTCTGTTGGGAGAGAGAGACCCAGCAAAATATGTACAAAGACATC 1887
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4379 TCAC-----GGAGCCAGACAACCAAGAAAGTACGTGACAGACATCTCTG 4423
Oy 1888 CAGCTTCATGGCCAGAGTGGCGAGAAATCTCTCCAGAGAACAGCCATATTTATGTG 1947
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4424 CAGAGCAGCTGGCGAGATCTGTGTACGAGCGCTGAAGAGAGCAAGGGGCCACATATAC 4483
Oy 1948 TGTGAGATGCAAAAGATATGCGCAAGATGTACATGATGCCCTTGTCAAAATATTAAGC 2007
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4484 GTCTGTGGGAGAGTACCATGCTGTGATGTCTCAAGCATCCAGCGCATCTATGACC 4543
Oy 2008 AAAGAGTTGGAGTTGAAAACTAGAGCAATGAAACCTGCGCATTAAAGAGAAA 2067
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4544 CAGCAGGGGAAAGCTCTCGGAGAGAGCGCGCGTATTCATCAGCGGATGAGGATGAC 4603
Oy 2068 AAAGCTACCTTCAGATATTT 2089
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4604 AACCATACATGAGATATTT 4625
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 6
US-09-123-708-3

Sequence 3, Application US/09123708

Patent No. 6148887

GENERAL INFORMATION:

APPLICANT: SCHRAEDER, Juergen

APPLICANT: GODECKE, Axel

TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC

FILE REFERENCE: 511169-2003

CURRENT APPLICATION NUMBER: US/09/123,708

CURRENT FILING DATE: 1998-07-28

EARLIER APPLICATION NUMBER: 08/553,503

EARLIER FILING DATE: 1996-03-01

EARLIER APPLICATION NUMBER: P4411402.8

EARLIER FILING DATE: 1994-03-31

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 4780

TYPE: DNA

ORGANISM: Cytomegalovirus

US-09-123-708-3

Query Match 3.0%; Score 63.6; DB 3; Length 4780;

Best Local Similarity 48.8%; Pred. No. 6.1e-10;

Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

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Oy 1588 TTCACCTTACAGATGACCCCTCAATCCCATCATATGATGGGTCCAGAAACCGGCATTA 1647
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4142 TTCACCTTACAGATGACCCCTCAATCCCATCATATGATGGGTCCAGAAACCGGCATTA 4201
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Db 4142 TTCACCTTACAGATGACCCCTCAATCCCATCATATGATGGGTCCAGAAACCGGCATTA 4201

Oy 1648 GCCCGGTTATTTGGTTCCTCAACATAGAGAAATCCCAAGAACACACCCAGATGGA 1707

Db 4202 GCCCGGTTATTTGGTTCCTCAACATAGAGAAATCCCAAGAACACACCCAGATGGA 4258

Oy 1708 AATTTTGAGCAATGTGTTGTTTGGCTGACAGGCAATAGATAGGATTAATCTATTC 1767

Db 4259 AACCCTTCCCATGCTCTGCTGCTTGGGTGCGGCAATCCAGATAGATCATATCTAC 4318

Oy 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGAGATCTTAAGTCAATCAAGGTTTCCTTC 1827

Db 4319 AGGAGAGAGACCTTCAGAGCCAGAGAACAGGGGGTCTTACAGAGACTGTACACGGCTTAC 4378

Oy 1828 TCAGAGATGCTCTCTGTTGGGAGAGAGAGACCCAGCAAAATATGTACAAAGACATC 1887

Db 4379 TCAC-----GGAGCCAGACAACCAAGAAAGTACGTGACAGACATCTCTG 4423

Oy 1888 CAGCTTCATGGCCAGAGTGGCGAGAAATCTCTCCAGAGAACAGCCATATTTATGTG 1947

Db 4424 CAGAGCAGCTGGCGAGATCTGTGTACGAGCGCTGAAGAGAGCAAGGGGCCACATATAC 4483

Oy 1948 TGTGAGATGCAAAAGATATGCGCAAGATGTACATGATGCCCTTGTCAAAATATTAAGC 2007

Db 4484 GTCTGTGGGAGAGTACCATGCTGTGATGTCTCAAGCATCCAGCGCATCTATGACC 4543

Oy 2008 AAAGAGTTGGAGTTGAAAACTAGAGCAATGAAACCTGCGCATTAAAGAGAAA 2067

Db 4544 CAGCAGGGGAAAGCTCTCGGAGAGAGCGCGCGTATTCATCAGCGGATGAGGATGAC 4603

Oy 2068 AAAGCTACCTTCAGATATTT 2089

Db 4604 AACCATACATGAGATATTT 4625

RESULT 7
US-09-123-624-3

Sequence 3, Application US/09123624

Patent No. 6149936

GENERAL INFORMATION:

APPLICANT: SCHRAEDER, Juergen

APPLICANT: GODECKE, Axel

TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

FILE REFERENCE: 511169-2004

CURRENT APPLICATION NUMBER: US/09/123,624

CURRENT FILING DATE: 1998-07-28

PRIOR APPLICATION NUMBER: 08/553,503

PRIOR FILING DATE: 1996-03-01

PRIOR APPLICATION NUMBER: 4411402.8

PRIOR FILING DATE: 1994-03-31

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 4780

TYPE: DNA

ORGANISM: Homo sapiens

US-09-123-624-3

Query Match 3.0%; Score 63.6; DB 3; Length 4780;

Best Local Similarity 48.8%; Pred. No. 6.1e-10;

Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

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Oy 1588 TTCACCTTACAGATGACCCCTCAATCCCATCATATGATGGGTCCAGAAACCGGCATTA 1647
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Db 4142 TTCACCTTACAGATGACCCCTCAATCCCATCATATGATGGGTCCAGAAACCGGCATTA 4201
Oy 1648 GCCCGGTTATTTGGTTCCTCAACATAGAGAAATCCCAAGAACACACCCAGATGGA 1707
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4202 GCCCGGTTATTTGGTTCCTCAACATAGAGAAATCCCAAGAACACACCCAGATGGA 4258
Oy 1708 AATTTTGAGCAATGTGTTGTTTGGCTGACAGGCAATAGATAGGATTAATCTATTC 1767
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 4259 AACCCCTGCCCCATGCTCTGCTCTGCGGTGCGCGCAATCCAGATGATCATATCTAC 4318
Qy 1768 AGAAAGAGCTCAGACATTTCTTAAAGCATGGATCTTAACATCATTAAGGTTTCCTTC 1827
Db 4339 AGGGAAGAGACCCCTGAGGCCAAGAGGAGGCTTTCAGAGAGCTGTACACGGCTTAC 4378
Qy 1828 TCAGAGATGCTCTGTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1887
Db 4379 TCCC-----GGAGCCAGACAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4423
Qy 1888 CAGCTTCATGGCCAGCAG 1947
Db 4424 CAGAGAGAGCTGGCGGAGCTCTGTGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4483
Qy 1948 TGTGAGATGCAAGAAATATGCGCAAGAGATGATGATGATGATGATGATGATGATGAT 2007
Db 4484 GTCTGTGGGAGAGCTGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4543
Qy 2008 AAAGAGTTGGATGTAAGAACTAGAGCAATGAAAGAGAGAGAGAGAGAGAGAGAGAG 2067
Db 4544 CAGCAGGGAGAGCTCTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4603
Qy 2068 AAAGCTACTTCAGAGATATTT 2089
Db 4604 AACGATACCATGAGATATTT 4625

RESULT 8
US-08-880-342-20

: Sequence 20, Application US/08880342

: Patent No. 6218179

: GENERAL INFORMATION:

: APPLICANT: Webster, Keith A.

: APPLICANT: Bishopric, Nanette H.

: APPLICANT: Murphy, Brian

: APPLICANT: Laderoute, Keith R.

: APPLICANT: Green, Christopher J.

: TITLE OF INVENTION: Tissue Specific Hypoxia Regulated

: NUMBER OF SEQUENCES: 37

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Dehlinger & Associates

: STREET: 350 Cambridge Avenue, Suite 250

: CITY: Palo Alto

: STATE: CA

: COUNTRY: USA

: ZIP: 94306

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patentin Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/880,342

: FILING DATE: 23-JUN-1997

: CLASSIFICATION: 514

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: PCT/IB95/00996

: FILING DATE: 13-NOV-1995

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 08/365,486

: FILING DATE: 23-DEC-1994

: ATTORNEY/AGENT INFORMATION:

: NAME: Sholtz, Charles K.

: REGISTRATION NUMBER: 38,615

: REFERENCE/DOCKET NUMBER: 8255-0018.30

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (415) 324-0880

: TELEFAX: (415) 324-0960

: INFORMATION FOR SEQ ID NO: 20:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 4780 base pairs

: TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human NOS-SN gene, Nakane, et al,
INDIVIDUAL ISOLATE: FEBS Lett 316:175 (1993)
FEATURE:
NAME/KEY: CDS
LOCATION: 431..4732
US-08-880-342-20

Query Match 3.0%; Score 63.6; DB 4; Length 4780;
Best Local Similarity 48.8%; Pred. No. 6.1e-10;
Matches 245; Conservative 0; Mismatches 239; Indels 18; Gaps 2;

Qy 1588 TTCCACTTACAGATGACCCCTCAATCCCATATATGTTGGTCCAGAACCGCATTA 1647
Db 4142 TTCCAGCTGCCCCGGAACCCCAAGTCCCTGCATCTCTGTGGACGAGCAGCGCATTT 4201
Qy 1648 GCCCGTTATTTGGTTCTCTACACATAGAGAGAACTCCAGAACACCCAGATGGA 1707
Db 4202 GCCCTTTCCAGACCTTGTGGCAACAGCG---GCAATTTGATATCCAAACAAAGGAATG 4258
Qy 1708 AATTTGAGCAATGTGTTGTTTGGCTGAGAGCATTAAGAGATTAAGATTAATCTATTC 1767
Db 4259 AACCCCTGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4318
Qy 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAACATCTAAGAGTTTCTCTTC 1827
Db 4319 AGGGAAGAGACCTTGACAGGCCAAGAACAGAGGGGTCTTCAAGAGAGCTGACACGCTTAC 4378
Qy 1828 TCAGAGATGCTCTGTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1887
Db 4379 TCCC-----GGAGCCAGACAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4423
Qy 1888 CAGCTTCATGGCCAGCAGAGTGCGAGAAATCTCTCCAGAGAGAGAGAGAGAGAGAGAG 1947
Db 4424 CAGAGAGAGCTGGGGAGAGTCTGTACCGAGACCTGTAAGAGAGAGAGAGAGAGAGAG 4483
Qy 1948 TGTGAGATGCAAGAAATATGCGCAAGAGATGATGATGATGATGATGATGATGATGAT 2007
Db 4484 GTCTGTGGGAGAGCTGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4543
Qy 2008 AAAGAGTTGGATGTAAGAACTAGAGCAATGAAAGAGAGAGAGAGAGAGAGAGAGAG 2067
Db 4544 CAGCAGGGAGAGCTCTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4603
Qy 2068 AAAGCTACTTCAGAGATATTT 2089
Db 4604 AACGATACCATGAGATATTT 4625

RESULT 9
US-08-365-486A-12

: Sequence 12, Application US/08365486A

: Patent No. 5834306

: GENERAL INFORMATION:

: APPLICANT: Webster, Keith A.

: APPLICANT: Bishopric, Nanette H.

: TITLE OF INVENTION: Tissue Specific Hypoxia Regulated

: NUMBER OF SEQUENCES: 31

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Dehlinger & Associates

: STREET: 350 Cambridge Avenue, Suite 250

: CITY: Palo Alto

: STATE: CA

: COUNTRY: USA

: ZIP: 94306

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: rat bnos cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 349..4638
US-08-365-486A-12

Query Match 2.7%; Score 57.2; DB 2; Length 5057;
Best Local Similarity 48.0%; Pred. No. 7.8e-08;
Matches 241; Conservative 0; Mismatches 243; Indels 18; Gaps 2;

QY 1588 TTCACCTTACGATGACCCCTCATCCCATCATTAATGCTGGCTCCAGAACCCGCATTA 1647
DB 4048 TTCACCTTACGATGACCCCTCATCCCATCATTAATGCTGGCTCCAGAACCCGCATTA 1647
QY 1648 GCGCCGTTTATGGTCTCTACATAGAGAACTCCAGAACACACACCAGATGGA 1707
DB 4108 GCACCCCTTCGAAAGCTTCTGGCAACAGGAC---AATTGACATCCAAACACAAAGAAATG 4164
QY 1708 AATTTGGAGCATGTGCTTTTGGCTGACAGCATTAAGATAGGATTAATCTATTC 1767
DB 4165 AATCGTGCCCATGTCTGCTTCGGGTGTCGACATCAACATGATGATCATATCTAC 4224
QY 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGGGATCTTACTCATCTAAAGCTTTCCTTC 1827
DB 4225 AGAGAGGAGACCTTCAGGCTAAGAAACAAGGCGCTTTCAGAGACTGTACACTGCTAT 4284
QY 1828 TCACAGATGCTCTGTTGGGAGAGAGAACCCAGCAAGATGATGTACAAACAACATC 1887
DB 4285 TCCTCGGGAAC-----GGACAGGCCAAAGAAATATGTACAGAGACGTGCTG 4329
QY 1888 CAGCTTCATGGCCAGCAGGTGGCGAATCTCTCCAGAGAACGCCATATTATGTG 1947
DB 4330 CAGCAACAGCTGAGTGTGTGTACCGCGCTCGAAGAGACAGAGGCCACATTTAT 4389
QY 1948 TGTGAGATGCAAAATAATATGGCCCAAGATGTACATGATGCCCTTGTGCAATAATTAAGC 2007
DB 4390 GTCTGTGGGAGCTTACATGCGCCGCGCATGTCTCAAGACCATCCAGCAATTAATGACC 4449
QY 2008 AAAGAGTTGAGTTGAAATAATAGCAATGAACCCCTGGCACTTTAAAGAGAA 2067
DB 4450 CAGCAGGGGAAACTCTCAGAGAGAGACGCTGTGTATTCATCAGAGGCTGAGGATGAC 4509
QY 2068 AAACGCTACCTTCAGGATATTT 2089
DB 4510 AACCGTACACAGAGACATCT 4531

RESULT 10
US-08-880-342-12

Sequence 12, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Denlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: rat bnos cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 349..4638
US-08-880-342-12

Query Match 2.7%; Score 57.2; DB 4; Length 5057;
Best Local Similarity 48.0%; Pred. No. 7.8e-08;
Matches 241; Conservative 0; Mismatches 243; Indels 18; Gaps 2;

QY 1588 TTCACCTTACGATGACCCCTCATCCCATCATTAATGCTGGCTCCAGAACCCGCATTA 1647
DB 4048 TTCACCTTACGATGACCCCTCATCCCATCATTAATGCTGGCTCCAGAACCCGCATTA 1647
QY 1648 GCGCCGTTTATGGTCTCTACATAGAGAACTCCAGAACACACACCAGATGGA 1707
DB 4108 GCACCCCTTCGAAAGCTTCTGGCAACAGGAC---AATTGACATCCAAACACAAAGAAATG 4164
QY 1708 AATTTGGAGCATGTGCTTTTGGCTGACAGCATTAAGATAGGATTAATCTATTC 1767
DB 4165 AATCGTGCCCATGTCTGCTTCGGGTGTCGACATCAACATGATGATCATATCTAC 4224
QY 1768 AGAAAGAGCTCAGACATTTCTTAAGCATGGGATCTTACTCATTAAGGCTTTCCTTC 1827

Db 4225 AGAGGAGACCTCTCAGGCTAAGAAAGGCGCTCTTACAGAGCTGTACACTGCTAT 4284
1828 TCAGAGATGCTCCCTGTTGGGAGAGAGAGCCCGACGAATATGTACAGACATC 1887
Db 4285 TCCCGGAGAC-----GGACAGGCCAAGAAATATGTACAGAGCTGTG 4329
1888 CAGCTTACATGCGCAGAGTGGCGAGAAATCTCTCCAGAGAAAGCCATTTATGTG 1947
Db 4330 CAGGAACAGCTGGCTGTACGCTGTACCGCGCTGAAAGAGCAAGAGCCACATTTAT 4389
1948 TGTGAGATGCAAAATATGTGCGCAGAGATGTACATGATGCCCTTGTGCAATTAATG 2007
4390 GTCTGTGGGAGCTTACCATGCGCGCGATGCTCAAGGCCATCCAGCGCATTAATGAC 4449
2008 AAAGAGTTGGAGTTGAAAACTAGAACAAATGAAACCCCTGCGCCATTTAAAGAGAA 2067
Db 4450 CAGCAGGGGAAACTCTCAGAGAGAGACCTGTGTATTCATCAGAGCTGAGGATGAC 4509
2068 AAACGCTACCTTCAGAGATATT 2089
Db 4510 AACCGTACCAAGAGACATCT 4531

RESULT 11

US-07-642-002-1
; Sequence 1, Application US/07642002
; Patent No. 5268465

GENERAL INFORMATION:

APPLICANT: Bredt, David S.
APPLICANT: Huang, Paul M.
APPLICANT: Reed, Randall
APPLICANT: Snyder, Solomon H.
TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA: US/07/642,002
FILING DATE: 19910118
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107, 033576
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 296-5500
TELEFAX: (202) 296-7830
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 5108 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
TISSUE TYPE: Brain
FEATURE:
NAME/KEY: CDS

LOCATION: 400..4686
OTHER INFORMATION:
US-07-642-002-1

Query Match 2.7%; Score 57.2; DB 1; Length 5108;
Best Local Similarity 48.0%; Pred. No. 7.9e-08;
Matches 241; Conservative 0; Mismatches 243; Indels 18; Gaps 2;

QY 1588 TCCCACTTACAGATGACCCCTCATCCCATCATTAATGTTGGTCCAGAACCGGCTTA 1647
Db 4099 TTCCACTGCTCCGAACCCCGAGGTGCTTGCATGTTGGGCCAGGACATGCTATC 4158
QY 1648 GCCCGTTTATTTGGTCTCTCAACATAGAGAGAAATCTCAAGAAACACCCAGATGA 1707
Db 4159 GCACCTTCCGAAGCTTGTGGCAACAGGAC---AATTGACATCCAAACACAAAGATG 4215
QY 1708 AATTGGAGCAATGTGTTGTTTGGCTGACAGCATTAAGATAGGATATATCTATTC 1767
Db 4216 AATCCGTGCCCATGTTCTGTGCTTCGGGTGTCGACAAATCCAAAGATGATCATATC 4275
QY 1768 AGAAAGAGCTCAGACATTTCTTACGATGCGATCTTAAGCATCTAAAGGTTCTTC 1827
Db 4276 AGAGAGAGACCTGCAAGGCTAAGACAAAGGCGTTTCAGAGAGCTGTACACTGCTAT 4335
QY 1828 TCAGAGATGCTCTGTTGGGAGAGAGAGCCCGACGAAGTATGTACAGACATC 1887
Db 4336 TCCCGGAGAC-----GGACAGGCCAAGAAATATGTACAGAGCTGTG 4380
QY 1888 CAGCTTACATGCGCAGCAGGTGGCGAGAAATCTCTCCAGAGAAAGCCCATTTATGTG 1947
Db 4381 CAGGAACAGCTGGCTGTGCTGTGTACCGCGCTGGAAGAGCAAGAGGCGCACATTTAT 4440
QY 1948 TGTGAGATGCAAAAGATATGCGCAAGATGTGATGCGCTTGTGCAATATATATG 2007
Db 4441 GTCTGTGGGAGCTTACCATGCGCCCATGTCTTCAAGCCATTCAGCGCATATATGAC 4500
QY 2008 AAAGAGTTGGAGTTGAAAACTAGAACAAATGAAACCCCTGCGCCATTTAAAGAGAA 2067
Db 4501 CAGCAGGGGAAACTCTCAGAGAGAGACCTGTGTATTCATCAGAGCTGAGGATGAC 4560
QY 2068 AAACGCTACCTTCAGAGATATT 2089
Db 4561 AACCGTACCAAGAGACATCT 4582

RESULT 12

US-09-627-216A-13
; Sequence 13, Application US/09627216A
; Patent No. 6368837

GENERAL INFORMATION:

APPLICANT: Sariastani, Sima F
APPLICANT: Tang, Xiao-Song
APPLICANT: Qi, Wei
APPLICANT: Vannelli, Todd
APPLICANT: Galenby, Anthony
TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
FILE REFERENCE: BC1009 US NA
CURRENT APPLICATION NUMBER: US/09/627,216A
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/147,719
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 13

LENGTH: 1863
TYPE: DNA
ORGANISM: Helianthus tuberosus
US-09-627-216A-13

Query Match 2.6%; Score 53.6; DB 4; Length 1863;
Best Local Similarity 48.8%; Pred. No. 6e-07;
Matches 254; Conservative 0; Mismatches 239; Indels 27; Gaps 3;

OY	1576	ACAAACAATTCCTCCCACTTACGAGTAGACCCCCTCATGCCCATCATTAATGTGGGTCCA	1635
Dd	1276	AGAACATCGAAGCTTCACAGCTCCAGGTCBACCCTTAAGTCCCGGTTATCATATTGGCCTT	1335
OY	1636	GGAACCGGCATAGCCCCGTTTTATTGGTTCCTCAACATAGAGAAACTCCAGAACA	1695
Dd	1336	GGAACCGGGTGCGCCCGTTAGAGGTTTTCTCAAGAAATTAAGCTCAAGGAATCT	1395
OY	1696	CACCCAGATGSAATTTTGGAGCAATGCGTGTGTTTTGGCTCGAGCATAAGAGTATAG	1755
Dd	1396	GGAACCGGAC-----TGGTCAATCCATTTTGTTCCTCGGTTCCAGAAACCGTAAGTG	1449
OY	1756	GATTATCTATTACAAAAAGAGCTCAGACATTTTCTTAAGCATGGGATCTTAACATCTA	1815
Dd	1450	GATTCATATATATGAGATGAACGAACACTTGTGTAAATGGCGGCTTTCCGAGCTT	1509
OY	1816	AAGTTTCTCTCCCAAGATAGCTCTGTTGGGAGAGAAAGCCCAAGCAAAATATCTA	1875
Dd	1510	GACATGGCTTTCTTCGC-----GAAGCGCATCTAAAGAAATACGTG	1551
OY	1876	CAAGACAACATCCAGCTTCATGGCCAGCAGGTGGCGAGAAATCTCTCCACAGAGAACGGC	1935
Dd	1552	CACATCTAAATAGACCCAAAGAGCTTCGGATAT--ATGGAACATGCTTTCTGAGGAGCA	1608
OY	1936	CATTTTATGTGTGTGGAGATGCAAAAGAAATATGGCCAAAGATGTACATGATGCCCTTGTG	1995
Dd	1609	TACTTATACGTGTGTGTGATGCCCAAAGAGCATGCTTAAGATGTACACCGAACCTTTCAC	1668
OY	1996	CAATTAATTAAGCAAGAAGGTTGGATGTGAAAAATAGNAGCAATGAAGAAACCCCTGGCCACT	2055
Dd	1669	ACCATGTGCAAGAAACAGGGAATTTGGATTCCTCTAAGCAGAGAGCTATGTGAAGAT	1728
OY	2056	TTAAAGAGAAAAACGCTACCTTCAGAGATTTTGGTCAT	2095
Dd	1729	CTACAAATGTGCGGAAGATFACCTCCGTGATGTTTGGTCAT	1768

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, RESULT 13
, US-09-134-001C-1557
, Sequence 1557, Application US/09134001C
, Patent No. 6380370
, GENERAL INFORMATION:
, APPLICANT: Lynn Doucette-Stamm et al
, TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
, TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
, FILE REFERENCE: GTC-007
, CURRENT APPLICATION NUMBER: US/09/134,001C
, PRIOR FILING DATE: 1998-08-13
, PRIOR APPLICATION NUMBER: US 60/064,964
, PRIOR FILING DATE: 1997-11-08
, PRIOR APPLICATION NUMBER: US 60/055,779
, PRIOR FILING DATE: 1997-08-14
, NUMBER OF SEQ ID NOS: 5674
, SEQ ID NO 1557
, LENGTH: 1890
, TYPE: DNA
, ORGANISM: Staphylococcus epidermidis
, US-09-134-001C-1557

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Query Match	2.58;	Score 52.8;	DB 4;	Length 1890;
Best Local Similarity	49.28;	Pred. NO. 1.1e-06;		
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[illegible]

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Oy	1734	TGCGTCGACGCGATPAGGATPAGGGATTTCATATTCAGAAAAGAGCTCAGACATTTTCCTTAA	1793
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Oy	1794	GCATGGGATCTTAACCTCATCTPAAAGGTTTCCCTCTCAAGAGATCCTCTGTGGGGAGA	1853
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Oy	1854	GGAAGCCCCAGCAAGATGATGCAACAGACAACATCCAGCTTCATGGCCAGCGAGTGGCGAG	1913
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Oy	1914	AATCCTCCTCCAGAGAAAGCGCCATTTATGTGTGTGGAGATSCAAAGAATATAGGCCAA	1973
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Oy	1974	GGATGTACATGATCCCTTGTGCAAAATATATAGCAAAAGAGGTTGGAGTTGAAAAACATAGA	2033
Db	1770	GGAGTTCATCTAACCGATTTAAAAATGTGTATATCAAAGAGCAAAAACCTATCTGAACAGA	1829
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Db	1830	TGCAGAGCAATCTTAAAAACAATGAAAAAGAGATPAAAAAGATATC 1873	

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1      RESULT 14
2      US-08-936-165A-113
3      ; Sequence 113, Application US/08936165A
4      ; Patent No. 6348582
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Black, Michael
7      ; APPLICANT: Burnham, Martin
8      ; APPLICANT: Hodgson, John
9      ; APPLICANT: Knowles, David
10     ; APPLICANT: Lonetto, Michael
11     ; APPLICANT: Nicholas, Richard
12     ; APPLICANT: Pratt, Julie
13     ; APPLICANT: Reichard, Richard
14     ; APPLICANT: Rosenberg, Martin
15     ; APPLICANT: Ward, Judith
16     ; TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
17     ; TITLE OF INVENTION: Polypeptides and Their Uses
18     ; NUMBER OF SEQUENCES: 534
19     ; CORRESPONDENCE ADDRESS:
20     ; ADDRESSEE: SmithKline Beecham Corporation
21     ; STREET: 709 Swedeland Road
22     ; CITY: King of Prussia
23     ; STATE: PA
24     ; COUNTRY: USA
25     ; ZIP: 19406-0939
26     ; COMPUTER READABLE FORM:
27     ; MEDIUM TYPE: Diskette
28     ; COMPUTER: IBM Compatible
29     ; OPERATING SYSTEM: DOS
30     ; SOFTWARE: FASTSEQ for Windows Version 2.0
31     ; CURRENT APPLICATION DATA:
32     ; APPLICATION NUMBER: US/08/936,165A
33     ; FILING DATE: 24-SEP-1997
34     ; CLASSIFICATION: 536
35     ; PRIOR APPLICATION DATA:
36     ; APPLICATION NUMBER: 60/027,032
37     ; FILING DATE: 24-SEP-1996
38     ; ATTORNEY/AGENT INFORMATION:
39     ; NAME: Gimmì, Edward R
40     ; REGISTRATION NUMBER: 38,891
41     ; REFERENCE/DOCKET NUMBER: P50549
42     ; TELECOMMUNICATION INFORMATION:
43     ; TELEPHONE: 610-270-4478
44     ; TELEFAX: 610-270-5090
45     ; TELEX:
46     ; INFORMATION FOR SEQ ID NO: 113:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1448 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
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US-08-936-165A-113

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Query Match      2.4%; Score 50.2; DB 4; Length 1448;
Best Local Similarity 58.3%; Pred. NO. 6.6e-06;
Matches 88; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
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Qy	1339	ATTATATGCTGTGGAGATGCAAAAGAAATTTGGCCAAAGATGTACATGATGACCTTGTCGA	1998
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Qy	1999	ATTATTAAGCAAGAGTGGAGCTTGAAATAACTAGACGATGAATAAACCCCTGGCCACTTTA	2055
Db	176	GTAATTTGGTAAAGAACGTCATATTTTCTCAGACAGACGAGATTTATTGCGACAAATG	235
Qy	2059	AAAGACAGAAAAACCGTACCTTCAGAGATATTT	2089
Db	236	AAACACACACACGCTATACACGAGATGTTT	266

RESULT 15
 US-09-302-620B-82
 Sequence 82, Application US/09302620B
 Patent No. 6331420
 GENERAL INFORMATION:
 APPLICANT: Wilson, C. Ron
 APPLICANT: Craft, David L.
 APPLICANT: Ehrlich, Dudley
 APPLICANT: Eshoo, Mark
 APPLICANT: Madduri, Krishna M.
 APPLICANT: Cornett, Cathy A.
 APPLICANT: Brenner, Alfred A.
 APPLICANT: Tang, Maria
 APPLICANT: Loper, John C.
 APPLICANT: Gleeson, Martin
 TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
 TITLE OF INVENTION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
 TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
 TITLE OF INVENTION: RELATING THERETO
 FILE REFERENCE: 1010-16 seq
 CURRENT APPLICATION NUMBER: US/09/302,620B
 CURRENT FILING DATE: 1999-04-30
 NUMBER OF SEQ ID NOS: 109
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 82
 LENGTH: 4145
 TYPE: DNA
 ORGANISM: Candida tropicalis
 US-09-302-620B-82

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QY	1648	GCCCCGTTTATTTGGGTTCTCAACATAGAGAGAACTCCAAAGAACAACCCAGATGA	1707
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Db	2701	AATGTGGCAAGACTTTGTTGTTTTTATGTGTGCAGAAACTCCACAGAGACTTTTTTTGAC	2760
QY	1768	AGAAAGA	1775

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2003, 10:56:19 ; Search time 424.476 Seconds
(without alignments)
10177.082 Million cell updates/sec

Title: US-09-371-347A-45

Perfect score: 2094

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Searched: 1439767 seqs, 1031500376 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2094	100.0	2094	US-09-371-347-45	Sequence 45, Appl
2	2081	99.4	2097	US-09-371-347-1	Sequence 1, Appl
3	2081	99.4	3259	US-09-371-347-24	Sequence 24, Appl
4	2079.4	99.3	2097	US-09-371-347-41	Sequence 41, Appl
5	2079.4	99.3	2097	US-09-371-347-43	Sequence 43, Appl
6	2063	98.5	2093	US-09-371-347-43	Sequence 43, Appl
7	174.4	8.3	2475	US-09-909-5678-38	Sequence 38, Appl
8	83.6	4.0	1872	US-09-917-800A-1351	Sequence 1351, Ap
9	83.6	4.0	2401	US-09-917-800A-1357	Sequence 1357, Ap
10	67.8	3.2	101	US-09-783-590-1364	Sequence 1364, Ap
11	62.4	3.0	298	US-09-294-093B-4842	Sequence 4842, Ap
12	58.2	2.8	230	US-09-923-876-2845	Sequence 2845, Ap
13	58.2	2.8	1863	US-09-765-873A-13	Sequence 13, Appl
14	56.2	2.7	2470	US-09-822-849A-278	Sequence 278, Appl
15	54.2	2.6	2136	US-09-938-842A-803	Sequence 803, Appl
16	51.4	2.5	2403	US-09-880-107-5039	Sequence 3039, Ap

17	50.6	2.4	4957	15	US-10-201-213-1	Sequence 1, Appl1
18	50.4	2.4	13508	8	US-08-781-966A-120	Sequence 120, App
19	50.2	2.4	1448	10	US-09-939-980-113	Sequence 113, App
20	48.8	2.3	411	10	US-09-925-289-440	Sequence 440, App
21	48.8	2.3	411	11	US-09-925-289-440	Sequence 440, App
22	47.6	2.3	1791	11	US-09-778-319-1	Sequence 1, Appl1
23	47.6	2.3	2088	11	US-10-128-714-7234	Sequence 7234, Ap
24	46	2.2	640681	15	US-09-790-988-1	Sequence 1, Appl1
25	44	2.1	2145	15	US-10-128-714-6234	Sequence 6234, Ap
26	44	2.1	3845	15	US-10-128-714-6234	Sequence 234, App
27	44	2.1	4145	15	US-10-128-714-5234	Sequence 5234, App
28	42.4	2.0	413	12	US-09-918-995-32917	Sequence 32917, A
29	42.4	2.0	534	12	US-09-918-995-9812	Sequence 9812, Ap
30	42.4	2.0	1254	11	US-09-989-920-10	Sequence 10, Appl
31	42.4	2.0	1845	15	US-10-128-714-1234	Sequence 1234, Ap
32	42.4	2.0	1845	15	US-10-128-714-2234	Sequence 2234, Ap
33	41.2	2.0	348	11	US-09-878-574-3001	Sequence 3001, Ap
34	40.6	1.9	382	10	US-09-956-004-78	Sequence 78, Appl
35	39.8	1.9	4056	15	US-10-156-761-2317	Sequence 2317, Ap
36	39.8	1.9	9025608	15	US-10-156-761-1	Sequence 1, Appl1
37	39.6	1.9	663	15	US-10-027-632-212141	Sequence 212141,
38	39.4	1.9	681	11	US-09-974-300-2079	Sequence 2079, Ap
39	39.2	1.9	396	12	US-09-918-995-4392	Sequence 4392, Ap
40	38.4	1.8	556	15	US-10-184-644-136	Sequence 136, App
41	38.4	1.8	556	15	US-10-184-644-136	Sequence 136, App
42	38.2	1.8	777	15	US-10-184-644-348	Sequence 348, App
43	38.2	1.8	777	15	US-10-184-644-348	Sequence 242, App
44	38	1.8	500	12	US-09-991-936-242	Sequence 242, App
45	37.8	1.8	1944	15	US-10-272-017A-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1	US-09-371-347-45	Sequence 45, Application US/09371347	
		Publication No. US20030082676A1	
	GENERAL INFORMATION:		
	APPLICANT: Roy A. Gravel et al.		
	TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:		
	TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE		
	TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER		
	FILE REFERENCE: 50004/003003		
	CURRENT APPLICATION NUMBER: US/09/371,347		
	CURRENT FILING DATE: 1999-08-10		
	PRIOR APPLICATION NUMBER: 60/071,622		
	PRIOR FILING DATE: 1998-01-16		
	PRIOR APPLICATION NUMBER: 09/232,028		
	PRIOR FILING DATE: 1999-01-15		
	NUMBER OF SEQ ID NOS: 51		
	SOFTWARE: FASTSEQ for Windows Version 4.0		
	SEQ ID NO 45		
	LENGTH: 2094		
	TYPE: DNA		
	ORGANISM: Homo sapiens		
	US-09-371-347-45		
Query Match	100.0%	Score 2094:	DB 12: Length 2094:
Best Local Similarity	100.0%	Pred. No. 0:	
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DB	61	GAATGTGAGCAAGCTGTGTACATGATTTTTCAGAGATCTTCACTGTATTGTGAA	120
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 1861 GCAAGATATGTACAGAACATATCCAGCTTATGAGCCAGAGTGGCCAGAAATCTCTCTC 1920
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RESULT 2
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 ; Sequence 1, Application US/09371347
 ; Publication No. US20030082676A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Roy A. Gravel et al.
 ; TITLE OF INVENTION: HUMAN METHYLONLINE SYNTHASE REDUCTASE:
 ; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
 ; FILE REFERENCE: 50004/003003
 ; CURRENT APPLICATION NUMBER: US/09/371,347
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: 60/071,622
 ; PRIOR FILING DATE: 1998-01-16
 ; PRIOR APPLICATION NUMBER: 09/232,028
 ; PRIOR FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 51
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LENGTH: 2097
TYPE: DNA
ORGANISM: Homo sapiens
US-09-371-347-1

Query Match 99.4%: Score 2081; DB 12; Length 2097;
Best Local Similarity 99.9%: Pred. No. 0;
Matches 2094; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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DB 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCAAATGTTTA 660
QY 661 ATTAAGAGCTTTGAGTCTCTACATTACCGTTGCGTACCCCACTCTCAGAGCCCTCTG 720
DB 661 ATTAAGAGCTTTGAGTCTCTACATTACCGTTGCGTACCCCACTCTCAGAGCCCTCTG 720
QY 721 AATATCTCGTGTATACCCCAAGAAATATTTACAGGTACATCTGACAGAGATCTCTGGCCAG 780
DB 721 AATATCTCGTGTATACCCCAAGAAATATTTACAGGTACATCTGACAGAGATCTCTGGCCAG 780
QY 781 GAGGAAGCCAAAGATCTGTGACTTACAGCATCCAGTTTTCAGAGTCCCAATTTCAAG 840
DB 781 GAGGAAGCCAAAGATCTGTGACTTACAGCATCCAGTTTTCAGAGTCCCAATTTCAAG 840
QY 841 CGAGTTCAACTTACTACGAATGATGCGATTAACCAACCACTGCTGCTGATTTGGAATTT 900
DB 841 CGAGTTCAACTTACTACGAATGATGCGATTAACCAACCACTGCTGCTGATTTGGAATTT 900
QY 901 TCAATATACGACTTTTCTATCAGCTTGAGATGCTTACAGCTGATCTGCCCTAACAGT 960

DB 901 TCAATATACGACTTTTCTATCAGCTTGAGATGCTTACAGCTGATCTGCCCTAACAGT 960
QY 961 GATTCGTGAGTACAAAGCTCTCCCAAGACTGACGTTGAAGTAAAGAGACACATGC 1020
DB 961 GATTCGTGAGTACAAAGCTCTCCCAAGACTGACGTTGAAGTAAAGAGACACATGC 1020
QY 1021 GTCCCTTTGAAATTAAGGCGACACAAAGAAAGAGAGCTTACCTTACCCACATATA 1080
DB 1021 GTCCCTTTGAAATTAAGGCGACACAAAGAAAGAGAGCTTACCTTACCCACATATA 1080
QY 1081 CCTGCGGAGTGTCTCTCAGCTTCAATTTTACCTGTGTCTTGAATTCGAGAAATTCCT 1140
DB 1081 CCTGCGGAGTGTCTCTCAGCTTCAATTTTACCTGTGTCTTGAATTCGAGAAATTCCT 1140
QY 1141 AAAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTGCATGCTGGAAGAGCGCAGG 1200
DB 1141 AAAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTGCATGCTGGAAGAGCGCAGG 1200
QY 1201 CTACAGAGCTGTGCAATTAACAAGGGGACCGCATTTTACCCGCTTGTACAGATGCC 1260
DB 1201 CTACAGAGCTGTGCAATTAACAAGGGGACCGCATTTTACCCGCTTGTACAGATGCC 1260
QY 1261 TGTGCTGTGCTGTGATCTCTCTCTGCTTCCCTTCTGTCAGACACACACTCAGTCTC 1320
DB 1261 TGTGCTGTGCTGTGATCTCTCTCTGCTTCCCTTCTGTCAGACACACACTCAGTCTC 1320
QY 1321 CTGCTCGACATCTTCTTAACTTCAACCCAGACCATTTGCTGTCAGAGTCAAGTTTA 1380
DB 1321 CTGCTCGACATCTTCTTAACTTCAACCCAGACCATTTGCTGTCAGAGTCAAGTTTA 1380
QY 1381 TTTACCCAGGAAAGCTCCATTTTGTCTTCAACATTTGGAATTTCTGTACTACGCCACA 1440
DB 1381 TTTACCCAGGAAAGCTCCATTTTGTCTTCAACATTTGGAATTTCTGTACTACGCCACA 1440
QY 1441 ACAGAGTTCTGCGGAGGAGATATGACAGCTGCGCTGCTGTTGTTGCTTCACTT 1500
DB 1441 ACAGAGTTCTGCGGAGGAGATATGACAGCTGCGCTGCTGTTGTTGCTTCACTT 1500
QY 1501 CTTGACGCAAAACATATCATGCCATCCCATGAACACAGCGGAAAGCCCTGCTTAAGATA 1560
DB 1501 CTTGACGCAAAACATATCATGCCATCCCATGAACACAGCGGAAAGCCCTGCTTAAGATA 1560
QY 1561 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC 1620
DB 1561 TCCATCTCTCTCGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC 1620
QY 1621 ATTAATGTGGGTCCAGAACCGGCAATGACCCCGTTTATTTGGGTTCTTCAACATAGAGAG 1680
DB 1621 ATTAATGTGGGTCCAGAACCGGCAATGACCCCGTTTATTTGGGTTCTTCAACATAGAGAG 1680
QY 1681 AAATCCCAAGAAACACCCAGATGGAATTTTGGAGCAATGTG---GTTTTTGGCTGC 1737
DB 1681 AAATCCCAAGAAACACCCAGATGGAATTTTGGAGCAATGTG---GTTTTTGGCTGC 1737
QY 1738 AGCATTAAGATAGGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGG 1797
DB 1738 AGCATTAAGATAGGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGG 1797
QY 1798 ATCTTAATCTCATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAACCC 1857
DB 1798 ATCTTAATCTCATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAACCC 1857
QY 1858 CCAGCAAGTATGTACAGACACATCCAGCTTCAATGACAGAGAGAGAGATCTCTC 1917
DB 1858 CCAGCAAGTATGTACAGACACATCCAGCTTCAATGACAGAGAGAGAGATCTCTC 1917
QY 1918 CTCCAGAGAACGCGCATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGGATGA 1977
DB 1918 CTCCAGAGAACGCGCATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGGATGA 1977
QY 1978 CATGATGCCCTTGTGCAAAATTAAGCAAGAGTTGAGTTGAAAACTAGAACCAATG 2037
DB 1978 CATGATGCCCTTGTGCAAAATTAAGCAAGAGTTGAGTTGAAAACTAGAACCAATG 2037

Db 1981 CATGATGCCCTTGTGCAATAATTAAGCAAGAGTTGGAGTTGAATAAAGCAATG 2040
Oy 2038 AAAACCTGGCCACTTTTAAAGAGAAAAAGCTACTCTTACAGATATTGGTCATTA 2094
Db 2041 AAAACCTGGCCACTTTTAAAGAGAAAAAGCTACTCTTACAGATATTGGTCATTA 2097

RESULT 3
US-09-371-347-24
; Sequence 24, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 3259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-24

Query Match 99.4%; Score 2081; DB 12; Length 3259;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2094; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Oy 1 ATGAGAGAGTTCTTCTTCTATATGCTACACAGCAGGAGGAGGAGCCATCGCAGAA 60
Db 80 ATGAGAGAGTTCTTCTTCTATATGCTACACAGCAGGAGGAGGAGCCATCGCAGAA 139
Oy 61 GAAATGTGTGAGCAAGCTGTGATCATGATTTTCTGAGATCTTCACTGATTTGTA 120
Db 140 GAAATGTGTGAGCAAGCTGTGATCATGATTTTCTGAGATCTTCACTGATTTGTA 199
Oy 121 TCCGATTAAGTATGACCTTAAACCGAAGACCTCTCTTGTGTGTGTTCTTACACAG 180
Db 200 TCCGATTAAGTATGACCTTAAACCGAAGACCTCTCTTGTGTGTGTTCTTACACAG 259
Oy 181 GGCACCGGAGACCCACCCGACAGCCCGCAAGTTTGTAAAGAAATACAGACCAACA 240
Db 260 GGCACCGGAGACCCACCCGACAGCCCGCAAGTTTGTAAAGAAATACAGACCAACA 319
Oy 241 CTGCGGTTGATTTCTTGTCTCACCTGCGGTATGGGTACTGGGTCTGGTATTCAGAA 300
Db 320 CTGCGGTTGATTTCTTGTCTCACCTGCGGTATGGGTACTGGGTCTGGTATTCAGAA 379
Oy 301 TACACCTACTTTTGCATGAGGAGGAGAAATTTGATAACAGACTTCAAGAGCTTGAGCC 360
Db 380 TACACCTACTTTTGCATGAGGAGGAGAAATTTGATAACAGACTTCAAGAGCTTGAGCC 439
Oy 361 CGGCAATTTCTATGACACTGAGACATGACATCTGTAGGTTTGAACCTTGTGGTTGAG 420
Db 440 CGGCAATTTCTATGACACTGAGACATGACATCTGTAGGTTTGAACCTTGTGGTTGAG 499
Oy 421 CCGTGATTTGCTGACCTGCGCAGCCCTCAGAAAAGCAATTTAGGTCAAGAGAGAA 480
Db 500 CCGTGATTTGCTGACCTGCGCAGCCCTCAGAAAAGCAATTTAGGTCAAGAGAGAA 559
Oy 481 GAGAGATTAAGTGGGAGCTCCGCTGGGATCACCCTGCTTGAAGACAGACCTTGTG 540
Db 560 GAGAGATTAAGTGGGAGCTCCGCTGGGATCACCCTGCTTGAAGACAGACCTTGTG 619
Oy 541 AAGTCAGAGCTGCTACACATTTGAATCTCAAGTCTGAGATTCGATGATTCAGAA 600

Db 620 AAGTCAGAGCTGCTACACATTTGAATCTCAAGTCCAGCTTCTGAGATTCGATTCAGAA 679
Oy 601 AGAAGGATTCGAGAGTTTGTAGAGCAAAATGCAAGTACAGACCAATTCATGTGTGA 660
Db 680 AGAAGGATTCGAGAGTTTGTAGAGCAAAATGCAAGTACAGACCAATTCATGTGTGA 739
Oy 661 ATTGAAGCTTTGAGTCCCTACCTTACCCGTTGGTATGCCCACTCTCAAGACCTCTGTG 720
Db 740 ATTGAAGCTTTGAGTCCCTACCTTACCCGTTGGTATGCCCACTCTCTGTG 799
Oy 721 AATATCTCGTTTATACCCCAAGATATTTTACAGTATCTGACAGAGTCTCTTGGCCAG 780
Db 800 AATATCTCGTTTATACCCCAAGATATTTTACAGTATCTGACAGAGTCTCTTGGCCAG 859
Oy 781 GAGGAAGCCCAAGTCTGCTGACCTTACAGATCCAGTTTTCAGAGTCCCAATTTCAAG 840
Db 860 GAGGAAGCCCAAGTCTGCTGACCTTACAGATCCAGTTTTCAGAGTCCCAATTTCAAG 919
Oy 841 GCAGTTCAACTTACTACGAATGATGCCATTAATAAACCACTCTGCTGTGAATTTGGACAT 900
Db 920 GCAGTTCAACTTACTACGAATGATGCCATTAATAAACCACTCTGCTGTGAATTTGGACAT 979
Oy 901 TCAATACAGACTTTTCTATACGCTGAGATGCTTACGCTGATCTGCCCTAACAGT 960
Db 980 TCAATACAGACTTTTCTATACGCTGAGATGCTTACGCTGATCTGCCCTAACAGT 1039
Oy 961 GATTTGTAGTACAAAGCTTACTCCAAAGACTGCAAGCTTTGAAGATTAAGAGACACTGC 1020
Db 1040 GATTTGTAGTACAAAGCTTACTCCAAAGACTGCAAGCTTTGAAGATTAAGAGACACTGC 1099
Oy 1021 GTCCCTTTGAATAATTAAGGAGACACAAAGAGAGAGGCTTACCTTACCCAGATTA 1080
Db 1100 GTCCCTTTGAATAATTAAGGAGACACAAAGAGAGAGGCTTACCTTACCCAGATTA 1159
Oy 1081 CCTGGGAGTCTCTCTCACTTATTTTACCTGCTGTGTGAATCCAGCAATTCCT 1140
Db 1160 CCTGGGAGTCTCTCTCACTTATTTTACCTGCTGTGTGAATCCAGCAATTCCT 1219
Oy 1141 AAAAGGATTTTGGCGCCCTTGTGACATATACAGTACAGTGTGAAAGAGGAGGAGG 1200
Db 1220 AAAAGGATTTTGGCGCCCTTGTGACATATACAGTACAGTGTGAAAGAGGAGGAGG 1279
Oy 1201 CTACAGAGCTGTGAGTAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
Db 1280 CTACAGAGCTGTGAGTAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1339
Oy 1261 TGTGCTCTCTTGTGATCT 1320
Db 1340 TGTGCTCTCTTGTGATCT 1399
Oy 1321 CTGCTGCAACATCTTCTTAACTTCAACCCAGACCATTTGCTGCAAGGCTCAAGTTTA 1380
Db 1400 CTGCTGCAACATCTTCTTAACTTCAACCCAGACCATTTGCTGCAAGGCTCAAGTTTA 1459
Oy 1381 TTTCAACCAGGAAGCTTCATTTTGTCTTCAACATTTGTGAATTTGTCTACTGACACA 1440
Db 1460 TTTCAACCAGGAAGCTTCATTTTGTCTTCAACATTTGTGAATTTGTCTACTGACACA 1519
Oy 1441 ACAGAGTCTTGGGAGAGGAGTATGACAGGCTGCGCTGCTGTTGTTGTTGCTTACGTT 1500
Db 1520 ACAGAGTCTTGGGAGAGGAGTATGACAGGCTGCGCTGCTGTTGTTGTTGCTTACGTT 1579
Oy 1501 CTTGACGCAACATACATGCAATCTCCATGAGACAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Db 1580 CTTGACGCAACATACATGCAATCTCCATGAGACAGGAGGAGGAGGAGGAGGAGGAGGAG 1639
Oy 1561 TCCATCTCTCTCTCAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
Db 1640 TCCATCTCTCTCTCAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
Oy 1621 ATATATGTTGGTCCAGAGACCGGAGATAGCCCTTTTATTTGGTCTCTAACAATAGAGAG 1680
Db 1700 ATATATGTTGGTCCAGAGACCGGAGATAGCCCTTTTATTTGGTCTCTAACAATAGAGAG 1759


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OY 1321 CTGCTCGAAGCATCTTCTAACTCAACCCAGACCATATTCGTGACAGCTCAAGTTTA 1380
    |||||||
Db 1321 CTGCTCGAAGCATCTTCTAACTCAACCCAGACCATATTCGTGACAGCTCAAGTTTA 1380
OY 1381 TTTCACCCAGGAAGTTCATTTTGTCTTCAACATTGTGGAATTTCTGTCTACTGCCACA 1440
    |||||||
Db 1381 TTTCACCCAGGAAGTTCATTTTGTCTTCAACATTGTGGAATTTCTGTCTACTGCCACA 1440
OY 1441 ACAGAGGTTCTGCGAAGGAGTATGTACAGGCTGGGCGCTTGTGTTCTTCACTCAGT 1500
    |||||||
Db 1441 ACAGAGGTTCTGCGAAGGAGTATGTACAGGCTGGGCGCTTGTGTTCTTCACTCAGT 1500
OY 1501 CTTCAGCCAAACATCATGATCCCATGAAGACAGCGGAAAGCCCTGGCTCTCAAGATA 1560
    |||||||
Db 1501 CTTCAGCCAAACATCATGATCCCATGAAGACAGCGGAAAGCCCTGGCTCTCAAGATA 1560
OY 1561 TCCATCTCTCTCGAAGCAAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC 1620
    |||||||
Db 1561 TCCATCTCTCTCGAAGCAAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC 1620
OY 1621 ATAAATGTTGGTTCAGGAACCGGATAGCCCGCTTATTTGGTCTTCAACATAGAGAG 1680
    |||||||
Db 1621 ATAAATGTTGGTTCAGGAACCGGATAGCCCGCTTATTTGGTCTTCAACATAGAGAG 1680
OY 1681 AAATCTCAGAAACACACCAGATGGAATTTTGGAGCAATGTG--GTTTTTGGCTGC 1737
    |||||||
Db 1681 AAATCTCAGAAACACACCAGATGGAATTTTGGAGCAATGTG--GTTTTTGGCTGC 1740
OY 1738 AGGCAATAGGATAGGAGTTATCTTCAAGAAAGGCTCAGACATTTCTTCAAGATGGG 1797
    |||||||
Db 1741 AGGCAATAGGATAGGAGTTATCTTCAAGAAAGGCTCAGACATTTCTTCAAGATGGG 1800
OY 1798 ATCTTAACATCTAAAGGTTTCTTCTCAAGAGATGCTCCGTTGGGAGAGAGAACCC 1857
    |||||||
Db 1801 ATCTTAACATCTAAAGGTTTCTTCTCAAGAGATGCTCCGTTGGGAGAGAGAACCC 1860
OY 1858 CCAGCAAAAGTATGTCAAGACACATCCAGCTTCAATGGCCAGAGTGCGAGAACTCTC 1917
    |||||||
Db 1861 CCAGCAAAAGTATGTCAAGACACATCCAGCTTCAATGGCCAGAGTGCGAGAACTCTC 1920
OY 1918 CTCCGAGGAAGCGGCATATTATGTGTGAGATGCAAAATATGSCCAAGATGTA 1977
    |||||||
Db 1921 CTCCGAGGAAGCGGCATATTATGTGTGAGATGCAAAATATGSCCAAGATGTA 1980
OY 1978 CATGATGCCCTTGTGCAATATATAGCAAGAGTGTGAGTTGAAAACTAGAACCATG 2037
    |||||||
Db 1981 CATGATGCCCTTGTGCAATATATAGCAAGAGTGTGAGTTGAAAACTAGAACCATG 2040
OY 2038 AAAACCCCTGGCCACTTTTAAAGAGAAAAAGCGTACCTTCAGGATATTTGGTCATTA 2094
    |||||||
Db 2041 AAAACCCCTGGCCACTTTTAAAGAGAAAAAGCGTACCTTCAGGATATTTGGTCATTA 2097

RESULT 5
US-09-371-347-43
; Sequence 43, Application US/09371347
; Publication No. US20030082676a1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE.
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 2097

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-43
Query Match      99.3%; Score 2079.4; DB 12; Length 2097;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY 1 ATGAGAGGTTCTCTTACTATATCTTACACAGCAGGAGCAGGCAAGGCCATCCGACAA 60
    |||||||
Db 1 ATGAGAGGTTCTCTTACTATATCTTACACAGCAGGAGCAGGCAAGGCCATCCGACAA 60
OY 61 GAAATGTGTAGACAGCTGTGTACATGATTTTGTGAGATCTTCACTGATTTAGTGA 120
    |||||||
Db 61 GAAATGTGTAGACAGCTGTGTACATGATTTTGTGAGATCTTCACTGATTTAGTGA 120
OY 121 TCCGATAGTATGACCTTAAACCAAGACGCTCTTGTGTTGTGTTGTTTACACAG 180
    |||||||
Db 121 TCCGATAGTATGACCTTAAACCAAGACGCTCTTGTGTTGTGTTGTTTACACAG 180
OY 181 GGCACCGGAGACCCACCCGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
    |||||||
Db 181 GGCACCGGAGACCCACCCGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
OY 241 CTGCCGTTGATTTCTTCTACCTGGGATGAGGTTACTGAGTCTCGTGTATCAGAA 300
    |||||||
Db 241 CTGCCGTTGATTTCTTCTACCTGGGATGAGGTTACTGAGTCTCGTGTATCAGAA 300
OY 301 TACACCTTCTTGTGAATGGGGGGAATATTTGATTAACGACTTCAAGAGCTTGGAGCC 360
    |||||||
Db 301 TACACCTTCTTGTGAATGGGGGGAATATTTGATTAACGACTTCAAGAGCTTGGAGCC 360
OY 361 CGGATTTCTATGACATGAGCATGACATGCTGTAGTTTGAAGTTGAGTTGAGTTGAG 420
    |||||||
Db 361 CGGATTTCTATGACATGAGCATGACATGCTGTAGTTTGAAGTTGAGTTGAGTTGAG 420
OY 421 CCGTGATTTCTGAGACTGTGGCCAGCCCTCAGAAAGCATTTTATAGTCAAGCAGAGACA 480
    |||||||
Db 421 CCGTGATTTCTGAGACTGTGGCCAGCCCTCAGAAAGCATTTTATAGTCAAGCAGAGACA 480
OY 481 GAGGAGATTAATGAGGCGACCTCCGCTGCTACCTGATCTGTAGAGATTTGAGATTTGAG 540
    |||||||
Db 481 GAGGAGATTAATGAGGCGACCTCCGCTGCTACCTGATCTGTAGAGATTTGAGATTTGAG 540
OY 541 AAGTACAGAGCTCTACATTAATCTCAAGTGCAGCTTCTGAGATTTGAGATTTGAG 600
    |||||||
Db 541 AAGTACAGAGCTCTACATTAATCTCAAGTGCAGCTTCTGAGATTTGAGATTTGAG 600
OY 601 AGAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTTGA 660
    |||||||
Db 601 AGAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTTGA 660
OY 661 ATGGAAGACTTGAATCTCTCACTTACCCGCTTGGTACCCCACTCTCAAGCCTCTGTG 720
    |||||||
Db 661 ATGGAAGACTTGAATCTCTCACTTACCCGCTTGGTACCCCACTCTCTCAAGCCTCTGTG 720
OY 721 AATATCTCTGTTTACCCCAAGATATTTTACAGATCACTGAGAGATCTCTTGGCCAG 780
    |||||||
Db 721 AATATCTCTGTTTACCCCAAGATATTTTACAGATCACTGAGAGATCTCTTGGCCAG 780
OY 781 GAGGAAGCCCAAGTATCTGTGACTTCAGCAGATCCAGTTTTCAAGTCCCAATTTCAAG 840
    |||||||
Db 781 GAGGAAGCCCAAGTATCTGTGACTTCAGCAGATCCAGTTTTCAAGTCCCAATTTCAAG 840
OY 841 GCAGTTCAACTTACTACGAATGATGCCATTAACCACTCTGCTGTGATTTGACACTT 900
    |||||||
Db 841 GCAGTTCAACTTACTACGAATGATGCCATTAACCACTCTGCTGTGATTTGACACTT 900
OY 901 TCAATATACAGACTTTTCTATACAGCTGAGAGTGTGCTTACAGCTGATTTGCCCTTACAG 960
    |||||||
Db 901 TCAATATACAGACTTTTCTATACAGCTGAGAGTGTGCTTACAGCTGATTTGCCCTTACAG 960
OY 961 GATTCTGAGGTACAAAGCCTACTCCAAAGACTGACGTTTGAAGATTAAGAGAGACTGC 1020
    |||||||

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Db 961 GATTCTGAGGTACAAAGCTTACTCCAAAGACTGACAGCTGAGAGTAAAGAGAGCACTGC 1020
OY 1021 GTTCCTTTGAAATAAAGGACACACAAGAAAGAGAGTACCTTACCACGACATATA 1080
Db 1021 GTTCCTTTGAAATAAAGGACACACAAGAAAGAGAGTACCTTACCACGACATATA 1080
OY 1081 CCTGGGGAGTGTCTCTCAGTTCATTTTACCTGGTGTCTGAAATCCGAGCAATTCCT 1140
Db 1081 CCTGGGGAGTGTCTCTCAGTTCATTTTACCTGGTGTCTGAAATCCGAGCAATTCCT 1140
OY 1141 AAAAAGGCAATTTTGGGAGCCCTTGTGACATATACAGTGTGACAGTGTGAAAAGCGCAG 1200
Db 1141 AAAAAGGCAATTTTGGGAGCCCTTGTGACATATACAGTGTGACAGTGTGAAAAGCGCAG 1200
OY 1201 CTACAGGACCTGTGACATTAACAAGGGGAGCCGATATAGCCGCTTGTAGAGATGCC 1260
Db 1201 CTACAGGACCTGTGACATTAACAAGGGGAGCCGATATAGCCGCTTGTAGAGATGCC 1260
OY 1261 TGTGCTGCTTGTGGATCTCCTCCGCTTCCCTTCCCTTCCGAGCCACACCTCAGTCTC 1320
Db 1261 TGTGCTGCTTGTGGATCTCCTCCGCTTCCCTTCCCTTCCGAGCCACACCTCAGTCTC 1320
OY 1321 CTGCTCGAACAATCTTCTAACTCAACCCAGACCATATTCGTGCAAGCTCAAGTTTA 1380
Db 1321 CTGCTCGAACAATCTTCTAACTCAACCCAGACCATATTCGTGCAAGCTCAAGTTTA 1380
OY 1381 TTTCACCCGAGAAAGCTCATTTTGTCTTCAACATTTGTGGAATTTGTCTCTACGACACA 1440
Db 1381 TTTCACCCGAGAAAGCTCATTTTGTCTTCAACATTTGTGGAATTTGTCTCTACGACACA 1440
OY 1441 ACAGAGTCTCTCGAAGGAGATGTATGTACAGGCTGCTGCTGCTTGTGTGCTTGCCTT 1500
Db 1441 ACAGAGTCTCTCGAAGGAGATGTATGTACAGGCTGCTGCTGCTTGTGTGCTTGCCTT 1500
OY 1501 GTTCAGCCAAACATATCATCTCCATGAAGACAGCGGAGAAAGCCCTGCTCCTAAGATA 1560
Db 1501 GTTCAGCCAAACATATCATCTCCATGAAGACAGCGGAGAAAGCCCTGCTCCTAAGATA 1560
OY 1561 TCCATCTCTCTCGAAGCAAAATTTCTTCACTTCCAGATGAGACCCCTCAATCCCATTC 1620
Db 1561 TCCATCTCTCTCGAAGCAAAATTTCTTCACTTCCAGATGAGACCCCTCAATCCCATTC 1620
OY 1621 ATATATGTTGGTTCAGGAACCGGACATAGCCCGTTTATTTGGTTCCTACACATAGAGAG 1680
Db 1621 ATATATGTTGGTTCAGGAACCGGACATAGCCCGTTTATTTGGTTCCTACACATAGAGAG 1680
OY 1681 AAATCTCAAGAACACACCCAGATGTGAAATTTTGAAGCAATGTG --GTTTGTGGCTGC 1737
Db 1681 AAATCTCAAGAACACACCCAGATGTGAAATTTTGAAGCAATGTG --GTTTGTGGCTGC 1737
OY 1738 AAGCATTAAGGATATGATATCTATTCAGAAAAGACTCAGACATTTCTTAAAGATGGG 1797
Db 1741 AAGCATTAAGGATATGATATCTATTCAGAAAAGACTCAGACATTTCTTAAAGATGGG 1800
OY 1798 ATCTTAATCATCTAAAGGTTTCTCTCTCAGAGATGTCTCTGTTGGGAGAGAGAGCC 1857
Db 1801 ATCTTAATCATCTAAAGGTTTCTCTCTCAGAGATGTCTCTGTTGGGAGAGAGAGCC 1860
OY 1858 CCAGCAAAATATGTACAGACACATCAGCTTCATGSCCAGCAGAGGTGCGAAGATCTTC 1917
Db 1861 CCAGCAAAATATGTACAGACACATCAGCTTCATGSCCAGCAGAGGTGCGAAGATCTTC 1920
OY 1918 CTCCAGGAGAGGCGCATTTTATGTGTGTGAGAGTGAAGAAATATGGCCAAAGATGTA 1977
Db 1921 CTCCAGGAGAGGCGCATTTTATGTGTGTGAGAGTGAAGAAATATGGCCAAAGATGTA 1980
OY 1978 CATGATGCCCTTGTGCAAAATATATAGCAAAAGAGTGTGAAAAGCTTAGAAGCAATG 2037
Db 1981 CATGATGCCCTTGTGCAAAATATATAGCAAAAGAGTGTGAAAAGCTTAGAAGCAATG 2040
OY 2038 AAAACCTTGCCCACTTTAAAGAGAAAAGCTTACCTTCAGAGATTTTGTGCTATTA 2094
|||||

Db 2041 AAAACCTTGCCCACTTTAAAGAGAAAAGCTTACTCTTCAGAGATTTTGTGCTATTA 2097
RESULT 6
US-09-371-347-47
; Sequence 47, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE.
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; PRIOR FILING DATE: 1999-08-10
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 2093
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-47

Query Match 98.5%; Score 2063; DB 12; Length 2093;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2090; Conservative 0; Mismatches 0; Indels 7; Gaps 2;

OY 1 ATGAGAGGTTTCTGTACTATATGCTACACAGCAGGAGGACGCAAGGCCATCGCAGAA 60
Db 1 ATGAGAGGTTTCTGTACTATATGCTACACAGCAGGAGGACGCAAGGCCATCGCAGAA 60
OY 61 GAAATGTGTGACCAAGCTGTGTACATGATGATTTTCTGAGATCTTCTACTGTATTAGTGA 120
Db 61 GAAATGTGTGACCAAGCTGTGTACATGATGATTTTCTGAGATCTTCTACTGTATTAGTGA 120
OY 121 TCCGATTAATGACTTAAACCGGAACGCTCCCTGTGTGTGTGTTCTTCTACAG 180
Db 121 TCCGATTAATGACTTAAACCGGAACGCTCCCTGTGTGTGTGTTCTTCTACAG 180
OY 181 GGCACCGGAGACCACCCGACACAGCCCGCAAGTTGTTAAGGAATATACGAACCAACA 240
Db 181 GGCACCGGAGACCACCCGACACAGCCCGCAAGTTGTTAAGGAATATACGAACCAACA 240
OY 241 CTGCGGTTGATTTCTTCTCCTCAGCTGCGGTATGGGTACTGGCTCTGCTGATTCAGAA 300
Db 241 CTGCGGTTGATTTCTTCTCCTCAGCTGCGGTATGGGTACTGGCTCTGCTGATTCAGAA 300
OY 301 TACACTACTTTTGCATATGGGGGAAGATTAATTAAGCAAGCTTCAAGAGCTTGAGCC 360
Db 301 TACACTACTTTTGCATATGGGGGAAGATTAATTAAGCAAGCTTCAAGAGCTTGAGCC 360
OY 361 CGCATTTTATAGACACTGACATGCAATGCACTGTGTAGACTTGTGAGTTGAGT 420
Db 361 CGCATTTTATAGACACTGACATGCAATGCACTGTGTAGACTTGTGAGTTGAGT 420
OY 421 CCGTGATTTCTGAGACTGTGCGCAGCCCTCAGAAAGCAATTTAGGTCAAGAGAGACAA 480
Db 421 CCGTGATTTCTGAGACTGTGCGCAGCCCTCAGAAAGCAATTTAGGTCAAGAGAGACAA 480
OY 481 GAGGAGATTAAGTGGCCCACTCCCGTGGCATACCTGTGATCTTGTAGAGACAGACTTGG 540
Db 481 GAGGAGATTAAGTGGCCCACTCCCGTGGCATACCTGTGATCTTGTAGAGACAGACTTGG 540
OY 541 AAGTCAGACTCTACATTAATTAATTAAGTCAAGTGTGAGCTTCTGAGATTTGATGATTCAGGA 600
Db 541 AAGTCAGACTCTACATTAATTAATTAAGTCAAGTGTGAGCTTCTGAGATTTGATGATTCAGGA 600
OY 601 AGAAGGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATTCATGTTGTA 660
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Db	601	AGAAAGATTCTGAGTTTTTGAAGCAAAATGCAGTAAACAGCAACCAATCCAATGTTGTA	660
QY	661	ATTGAAGACTTTGAGTCTCCTACTTACCCTGTGGGTACCCCACTCTCACAAAGCTCTCTG	720
Db	661	ATTGAAGACTTTGAGTCTCCTACTTACCCTGTGGGTACCCCACTCTCACAAAGCTCTCTG	720
QY	721	AATATTCGAGTTTACCCTCCAGAAATTTTACAGGTACATCTGAGAGTCTTGTGCCAG	780
Db	721	AATATTCGAGTTTACCCTCCAGAAATTTTACAGGTACATCTGAGAGTCTTGTGCCAG	780
QY	781	GAGGAAAGCCAGTATCTGTGACTTCAGAGATCCAGTTTTTCAATGTCCAAATTTCAAG	840
Db	781	GAGGAAAGCCAGTATCTGTGACTTCAGAGATCCAGTTTTTCAATGTCCAAATTTCAAG	840
QY	841	GCAGTTCAACTTACTACGAAATGATGCGATAAAAACACACTCTGCTGTAGAAATTTGACATT	900
Db	841	GCAGTTCAACTTACTACGAAATGATGCGATAAAAACACACTCTGCTGTAGAAATTTGACATT	900
QY	901	TCAAATACGACTTTTCCCTATCAGCTGAGATGCTTACGCTGATCTGCCCTAACAT	960
Db	901	TCAAATACGACTTTTCCCTATCAGCTGAGATGCTTACGCTGATCTGCCCTAACAT	960
QY	961	GATTTGAGGTACAAAGCCTTACTCCAAAGACACAGCTTGAAGATTTAAAGAGACACCTGC	1020
Db	961	GATTTGAGGTACAAAGCCTTACTCCAAAGACACAGCTTGAAGATTTAAAGAGACACCTGC	1020
QY	1021	GTCTTTTGAATAAAGGACAGACACAAAGAAAGAGACGTACCTTACCCTCCAGATATA	1080
Db	1021	GTCTTTTGAATAAAGGACAGACACAAAGAAAGAGACGTACCTTACCCTCCAGATATA	1080
QY	1081	CCTGGGGGATGTCTCTCCAGTTCATTTTACTGCTGTGCTGAATCCGAGACATTCTCT	1140
Db	1081	CCTGGGGGATGTCTCTCCAGTTCATTTTACTGCTGTGCTGAATCCGAGACATTCTCT	1140
QY	1081	CCTGGGGGATGTCTCTCCAGTTCATTTTACTGCTGTGCTGAATCCGAGACATTCTCT	1140
Db	1081	CCTGGGGGATGTCTCTCCAGTTCATTTTACTGCTGTGCTGAATCCGAGACATTCTCT	1140
QY	1141	AAAAAGCATTTTTTTCGAGCCCTTGTGACATTTACAGTACGACAGTGTGAAAAGGCGAG	1200
Db	1141	AAAAAGCATTTTTTTCGAGCCCTTGTGACATTTACAGTACGACAGTGTGAAAAGGCGAG	1200
QY	1201	CTACAGGACCTGTGCAGTAAACAAAGGGGAGCCGATTTATAGCCGCTTTGTACGAGATGCC	1260
Db	1201	CTACAGGACCTGTGCAGTAAACAAAGGGGAGCCGATTTATAGCCGCTTTGTACGAGATGCC	1260
QY	1261	TGTGCTCTGTTTGGATCTCTCTCTGCTTCCCTTCTGTGCACACACACTCAGTCTC	1320
Db	1261	TGTGCTCTGTTTGGATCTCTCTCTGCTTCCCTTCTGTGCACACACACTCAGTCTC	1320
QY	1321	CTGCTCGAACAATCTTCTTAACTTAAACCCAGACCATATGCTGTGCAAGGCTCAAGTTTA	1380
Db	1321	CTGCTCGAACAATCTTCTTAACTTAAACCCAGACCATATGCTGTGCAAGGCTCAAGTTTA	1380
QY	1381	TTTTCACCCAGGAAGCTCATTTTGTCTTCAACATTTGTGAATTTCTGTACTGACCACA	1440
Db	1381	TTTTCACCCAGGAAGCTCATTTTGTCTTCAACATTTGTGAATTTCTGTACTGACCACA	1440
QY	1441	ACAGAGGTTTCGCGAAGGAGTATGTACAGGCTGTGCGCTTGTGTTGCTTCAAGTT	1500
Db	1441	ACAGAGGTTTCGCGAAGGAGTATGTACAGGCTGTGCGCTTGTGTTGCTTCAAGTT	1500
QY	1501	CTTCAGCCAAACATCATGCAATCCCATAAAGACAGCGGAAAGCCGTGGCTCCTAAGATA	1560
Db	1501	CTTCAGCCAAACATCATGCAATCCCATAAAGACAGCGGAAAGCCGTGGCTCCTAAGATA	1560
QY	1561	TCATCTCTCTCGAACAACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC	1620
Db	1561	TCATCTCTCTCGAACAACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC	1620
QY	1621	ATAATGTGGGTCCAGGAACCGCATAGCCCGTTTATTTGGGTCTTCAACATAGAGAG	1680
Db	1621	ATAATGTGGGTCCAGGAACCGCATAGCCCGTTTATTTGGGTCTTCAACATAGAGAG	1680
QY	1681	AAATCTCCAAAGAACACCCAGATGGAAATTTTGGAGCAATGTG- ---GTTTTTGGCTGC	1737
Db	1677	AAATCTCCAAAGAACACCCAGATGGAAATTTTGGAGCAATGTGTTTGGTGGCTGC	1736

QY	1738	AGCGATAAGGATAGGGATTATTCATTATCGAAGAAAGAGCTCAGACATTTCCTTAAGCATGGG	1797
Db	1737	AGGCAATAGGATAGGGATTATTCATTATTCAGAAAAGAGCTCAGACATTTCCTTAAGCATGGG	1796
QY	1798	ATCTTAACCATCATTAAGGTTCTCTTCACAGAGATGCTCCGTGTGGGAGGAGGAGAGCC	1857
Db	1797	ATCTTAACCATCATTAAGGTTCTCTTCACAGAGATGCTCCGTGTGGGAGGAGGAGAGCC	1856
QY	1858	CCAGCAAAAGTATGTACAGACACACATCCAGCTTCATGGCCAGCAGGTGGCGAATCCCTC	1917
Db	1857	CCAGCAAAAGTATGTACAGACACACATCCAGCTTCATGGCCAGCAGGTGGCGAATCCCTC	1916
QY	1918	CTCCAGGAGAGACGCCCATATTTATGTGTGTGGAGATGCAAAATAATATGSCCAAGGATGTA	1977
Db	1917	CTCCAGGAGAGACGCCCATATTTATGTGTGTGGAGATGCAAAATAATATGSCCAAGGATGTA	1976
QY	1978	CATGATGGCCCTGTGCAATAATATAAGCAAAAGAGTTGGAGTTGAAAACTAGAGCAATG	2037
Db	1977	CATGATGGCCCTGTGCAATAATAATAAGCAAAAGAGTTGGAGTTGAAAACTAGAGCAATG	2036
QY	2038	AAAAACCTGGCCACTTTAAAAAGAAAGAAAGCGCTACCTTCACAGATATTTTGGCATATA	2094
Db	2037	AAAAACCTGGCCACTTTAAAAAGAAAGAAAGCGCTACCTTCACAGATATTTTGGCATATA	2093

RESULT 7
US-09-909-567B-38

; Sequence 38, Application US/09909567B
; Publication No. US20030022257A1

```

: GENERAL INFORMATION:
:
: APPLICANT: Macina, Roberto A.
:
: ADDITIONAL: Nair, Manoel

```

APPLICANT: Chen, Seiyu
TITLE OF INVENTION: Compositions and Methods Relating to RNAi Specific Sequences

FILE REFERENCE: DEX -0214
CURRENT APPLICATION NUMBER: US/09/2909,567B

; CURRENT FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: 60/219,834

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; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 56

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 2425

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: ORGANISM: Homo sapiens
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: FEATURE:
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: NAME/KEY: misc feature

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; LOCATION: (1001)..(1001)
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; OTHER INFORMATION: a, c, g or t
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; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (1011)..(1011)
; OTHER INFORMATION: a, c, g or t

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05-09-909-567B-38

Query match	8.3%	Score 1/4.4;	DB 12;	length 2475;
Best Local Similarity	96.7%	Pred. No. 9e-45;		
Matches 178: Conservative	0:	Mismatches	5:	Indels
			0:	Gap

510 ATCACTGCATCTTGGAGGACAGACCTTGTGACACAGACAGACCTGTCACACATTTGCAATTCGCA 560
by 100% conservative 0; mismatches 0; indels 0; gaps 0;

Db 1 ATCACCCTGCATCTCGAGACACAGACCCTTGTGAAGTACAGAGCTTACACATTGAATCTCA 60

570 AGTCGAGCTTCGAGATTCGATTCGAGAACAAAGCATTCGAGGTTTGAAGCAAAA 629

Dp 61 AGTGGAGCTTCTGAGATTGAGATTGAGGAAGAAGATCTCTGAGCTTTGAGACAAA 120

630 TGCAGTGAACAGCAACCATCCATGCTGTAATTGAAGACTTTGAGTCCCTACTTACCCG 689

Db 121 TGCAGTGAACAGCAACCAATCCATGTTGTAATTGAAGACTTTGAGTCTCCTACGGGATCTC 180

QY 690 TPCG 693

; SEQ ID NO 4842

1654 TTTATTGGGTTCTTACAACATAGAGAGAACTCCAAGAACACACCAGATGGAATTTT 1713

Db 62 TTGAGAGCTTCTTGACAGAAAGTTAGCATTAACAATCTGGGAGCAATGGGCACT 121
Qy 1714 GGACCATGTGTTTTTGGCTGCAGCATAGGATAGGATATCTATTAGAAAAG 1773
Db 122 T--CAATCCTTTCTTTGGATGCGAAGCACTAATATGACTCATATGAGAGATG 178
Qy 1774 CTCAGACATTTCTTAAGCATGATCTTAACATCATTAAGGTTCTCTCT 1825
Db 179 TTGCATACTTCTTTGANGAGGGCGCTTCTGAGCTAATTTGTCATTCT 230

RESULT 13
US-09-765-873A-13
; Sequence 13, Application US/09765873A
; Patent No. US20010053847A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009 US CIP
; CURRENT APPLICATION NUMBER: US/09/765,873A
; PRIORITY FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/627,216
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Helianthus tuberosus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1764)
; US-09-765-873A-13

Query Match 2.8%; Score 58.2; DB 10; Length 1863;
Best Local Similarity 49.3%; Pred. No. 2.7e-07;
Matches 255; Conservative 0; Mismatches 238; Indels 24; Gaps 3;

Qy 1576 ACAACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATATATGTTGGTCA 1635
Db 1276 AGAACATCGAACCTTGACACTTCCAGCTGAACCTTAAGTCCCGTTATCATGTTGGCCT 1335
Qy 1636 GGAACCGGCATAGCCCCCTTATTTGGTTCTTACACATAGAGAAACTCCAACAA 1695
Db 1336 GGAACCGGCTTGGCTCCCTTGAAGAGTTTCTTCAAGAAATAGCTCTCAAGAACT 1395
Qy 1696 CACCAGATGAAATTTTGAGACATGTGTTTTTGGCTGAGCATAGAGATAGGAT 1755
Db 1396 GGAACCGA---ACTGGTCAATCATTTTGTCTTCCGTTGACAGAAACCGTAAGTGAT 1452
Qy 1756 TATCATTTAGAAAAGAGCTAGACATTTCTTAAGCATGGGATCTTAAGTCTAAAG 1815
Db 1453 TTCAATATATGAAATGAACTGAACAATTTGTTGAATGAGCGCTTTCCAGCTTGAC 1512
Qy 1816 GTTTCCTTCTCAAGATGCTCTCTTGGGAGAGGAAAGCCCGACAGAAATATGTACA 1875
Db 1513 ATGGCTTCTCTCGC-----GAAGCGCATCTTAAGAAATATGCTGCA 1554
Qy 1876 GACACATTCAGCTTCATGGCCAGGAGTGGGAGAAATCTCTCCAGAGAAAGCGCAT 1935
Db 1555 CATAAATGAGCCAAAGGCTTGGATAT---ATGAAACATCTTTCTGAGGAGACATAC 1611
Qy 1936 ATTATGTGTGTGAGATGCAAAATATGGCCAAAGATGATACATGATGCCCTTGTGCA 1995
Db 1612 TTATAGTGTGTGTGATGCCAAAGCATGGCTTAAGATGTACACCAACCTTCAACACC 1671
Qy 1996 AATAATAGCAAGAGCTTGTGAGATGAAAAACTAGAAAGCATAAACCTGGCCACTTTA 2055
Db 1672 ATTTGCAAGAAAGCAAGAAATTTGATCTCTTAAAGCAGACCTGTATGTGAAGATCTA 1731
Qy 2056 AAGAAGAAAGAGCTACCTTCAGATATTTGTCAT 2092

Db 1732 CAATGTGCGGAAGATACCTCGGTGATGTTGGTAT 1768

RESULT 14
US-09-822-849A-278
; Sequence 278, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukola, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; PRIORITY FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 278
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-822-849A-278

Query Match 2.7%; Score 56.2; DB 10; Length 2470;
Best Local Similarity 54.7%; Pred. No. 1.4e-06;
Matches 134; Conservative 0; Mismatches 108; Indels 3; Gaps 1;

Qy 1588 TTCCACTTACAGATGACCCCTCAATCCCATATATGTTGGTCCAGAAACCGGCATA 1647
Db 1615 TTCCGCTTCCCTTTAAGGCCACACGCTGTATCATATGTTGGTCCAGAAACCGGCATG 1674
Qy 1648 GCGCCGTTATTTGGTTCTTCAACATAGAGAAACTCCAAGAAACACCCAGATGGA 1707
Db 1675 GCACCTTCATATGCTTTCATCAGAGAGCGGCTGCTGCGCACAGGCAAGAGAGTG 1734
Qy 1708 AATTTTGAGCATGTGTTTTTGGCTGACAGGCAATAAGATAGGATATATATTCAGA 1767
Db 1735 GGG---GAGACCTCTCTTACTACGCTGCGCCGCTCGATGAGAGACTTACCTGTAACGG 1791
Qy 1768 AAGAGCTCAGACATTTCTTAAAGCATGGATCTTAAGCATCTTAAGGTTCTTCTCA 1827
Db 1792 GAGGAGCTGGCCAGCTTCCACAGGAGGAGGTGCGTCCACCGACTCAAGCTGCTTCTTC 1851
Qy 1828 AGAGA 1832
Db 1852 CGGGA 1856

RESULT 15
US-09-938-842A-803
; Sequence 803, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kieps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIORITY FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2003, 09:58:39 ; Search time 88.9321 Seconds
(without alignments)
7221.032 Million cell updates/sec

Title: US-09-371-347A-45
Perfect score: 2094

Sequence: 1 atgaggaggttcctgact.....ttcagatattggtcataa 2094

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTC05.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Dackfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2081	99.4	3259	4	US-09-318-448-23
2	386.4	18.5	390	4	US-08-905-223-71
3	58.2	2.8	1863	4	US-09-627-216A-13
4	57.4	2.7	4353	2	US-08-365-486A-18
5	57.4	2.7	4353	4	US-08-880-342-18
6	57.4	2.7	4780	2	US-08-365-486A-20
7	57.4	2.7	4780	3	US-09-123-708-3
8	57.4	2.7	4780	3	US-09-123-708-3
9	57.4	2.7	4780	4	US-08-880-342-20
10	52.6	2.5	5057	2	US-08-365-486A-12
11	52.6	2.5	5057	4	US-08-880-342-12
12	52.6	2.5	5108	4	US-07-642-002-1
13	50.2	2.4	1448	4	US-08-936-165A-113
14	49.4	2.4	1890	4	US-09-134-001C-1557
15	46.2	2.2	7218	1	US-08-232-463-14
16	45.6	2.2	7218	1	US-08-232-463-14
17	44	2.1	307	4	US-09-172-711-24
18	40.6	1.9	382	4	US-08-976-258-78
19	37.8	1.8	4145	4	US-09-302-620B-82
20	36.6	1.7	3701	1	US-08-553-279-1
21	36.6	1.7	4041	1	US-08-147-812-4
22	36.6	1.7	4110	3	US-09-123-708-1
23	36.6	1.7	4110	3	US-09-123-708-1
24	36.6	1.7	4165	1	US-08-147-812-6
25	36.6	1.7	4546	4	US-09-146-053-6
26	36.2	1.7	4206	4	US-09-302-620B-81
27	36	1.7	4089	1	US-07-908-245-1

28	36	1.7	4097	3	US-09-123-708-5	Sequence 5, Appl
29	36	1.7	4097	3	US-09-123-708-5	Sequence 5, Appl
30	35.4	1.7	1296	4	US-09-134-001C-1501	Sequence 1501, Ap
31	34.8	1.7	4062	4	US-09-126-109-11	Sequence 11, Appl
32	34.8	1.7	4145	1	US-08-314-917-1	Sequence 1, Appl
33	34.8	1.7	4145	1	US-08-265-046-1	Sequence 1, Appl
34	34.8	1.7	4145	2	US-08-465-522-1	Sequence 1, Appl
35	34.8	1.7	4145	5	PCR-US93-11401-1	Sequence 1, Appl
36	34.8	1.7	4145	5	PCR-US95-07849-1	Sequence 1, Appl
37	34.2	1.6	1569	3	US-08-680-726A-57	Sequence 57, Appl
38	34.2	1.6	1569	3	US-09-092-409-57	Sequence 57, Appl
39	34.2	1.6	10592	1	US-08-680-726A-51	Sequence 51, Appl
40	34.2	1.6	10592	1	US-08-680-726A-52	Sequence 52, Appl
41	34.2	1.6	10592	3	US-09-092-409-51	Sequence 51, Appl
42	34.2	1.6	10592	3	US-09-092-409-52	Sequence 52, Appl
43	34	1.6	2223	1	US-08-257-073-4	Sequence 4, Appl
44	33.8	1.6	1702	1	US-08-261-822A-14	Sequence 14, Appl
45	33.8	1.6	1702	5	PCR-US95-07744A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1						
US-09-318-448-23						
Sequence 23, Application US/09318448						
Patent No. 6210950						
GENERAL INFORMATION:						
APPLICANT: Johnson, William G.						
APPLICANT: Stearns, Edward S.						
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING						
FILE REFERENCE: 601-1-057						
CURRENT FILING DATE: 1999-05-25						
NUMBER OF SEQ ID NOS: 46						
SOFTWARE: PatentIn Ver. 2.0						
SEQ ID NO 23						
LENGTH: 3259						
TYPE: DNA						
ORGANISM: Homo sapiens						
US-09-318-448-23						
Query Match						
Best Local Similarity 99.9%: Pred. No. 0:						
Matches 2094: Conservative 0; Mismatches 0; Indels 3; Gaps 1:						
QY	1	ATGAGAGAGTTCTGTTACTATATGCTACACAGCAGGACGCAAGCCATCCAGAA	60			
DB	80	ATGAGAGAGTTCTGTTACTATATGCTACACAGCAGGACGCAAGCCATCCAGAA	139			
QY	61	GAATGTGTGACAGCAGCTGTGTACATGATTTTTCAGATCTTCACGTATTAGTGA	120			
DB	140	GAATGTGTGACAGCAGCTGTGTACATGATTTTTCAGATCTTCACGTATTAGTGA	199			
QY	121	TCGGAATGATGACCTAAACGCAACAGCTCTCTGTGTGTGTTCTTACACG	180			
DB	200	TCGGAATGATGACCTAAACGCAACAGCTCTCTGTGTGTGTTCTTACACG	259			
QY	181	GGCAGCGAGACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	240			
DB	260	GGCAGCGAGACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	319			
QY	241	CTGCGGTTGATTTTGTCTCACCCTGCGGATATGGCTTACTGCTCGCTGATTCAGAA	300			
DB	320	CTGCGGTTGATTTTGTCTCACCCTGCGGATATGGCTTACTGCTCGCTGATTCAGAA	379			
QY	301	TACACCTCTTTTGAATGGGGGAAGTAATGTAACGACTCAAGAGCTTGAGACC	360			
DB	380	TACACCTCTTTTGAATGGGGGAAGTAATGTAACGACTCAAGAGCTTGAGACC	439			
QY	361	CGGATTTCTATGACACTGACATGACATGACATGACATGACATGACATGACATGAC	420			

440 CGGATTTCTATGACATCTGACATGACATGACTGTGAGTTAGATTGAACCTGTGGTTGAG 499
QY 421 CCGTGGATTTGCTGAGACTCTGGCCAGCCCTCAGAAAGCATTTTAGTCAAGAGAGACAA 480
Db 500 CCGTGGATTTGCTGAGACTCTGGCCAGCCCTCAGAAAGCATTTTAGTCAAGAGAGACAA 559
QY 481 GAGGAGATTAAGTGGGCGACTCCCGGTGCGATCACCCTGCATCTTGAGSACAGACCTTGTG 540
Db 560 GAGGAGATTAAGTGGGCGACTCCCGGTGCGATCACCCTGCATCTTGAGSACAGACCTTGTG 619
QY 541 AAGTCAGAGCTGCTCAGACATTGAATCTCAAGCGAGCTTGAGATTGATGATGATGACGA 600
Db 620 AAGTCAGAGCTGCTCAGACATTGAATCTCAAGCGAGCTTGAGATTGATGATGATGACGA 679
QY 601 AGAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTTGA 660
Db 680 AGAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTTGA 739
QY 661 ATTGAAGACTTTGAGTCTCTCACTTACCCGTTGCGTACCCCACTCTCAAGACCTCTGTG 720
Db 740 ATTGAAGACTTTGAGTCTCTCACTTACCCGTTGCGTACCCCACTCTCAAGACCTCTGTG 799
QY 721 AATATTCCTGGTTTACCCCGCAAAATTTTACAGGTACATCTGCAAGAGATCTCTTGGCCAG 780
Db 800 AATATTCCTGGTTTACCCCGCAAAATTTTACAGGTACATCTGCAAGAGATCTCTTGGCCAG 859
QY 781 GAGCAAGCCCAAGTATCTGTGACTTCAAGCATCCAGTCTTCAAGTCCCAATTTCAAG 840
Db 860 GAGCAAGCCCAAGTATCTGTGACTTCAAGCATCCAGTCTTCAAGTCCCAATTTCAAG 919
QY 841 GCAGTTCACCTTACTACGATGATGATGCCATTAAGAACCACTGTGCTGTAAGATTGACAT 900
Db 920 GCAGTTCACCTTACTACGATGATGATGCCATTAAGAACCACTGTGCTGTAAGATTGACAT 979
QY 901 TCAATATCAGACTTTTCTATCAGGCTGAGATGCTTCAAGGATGATGCTTCAAGAT 960
Db 980 TCAATATCAGACTTTTCTATCAGGCTGAGATGCTTCAAGGATGATGCTTCAAGAT 1039
QY 961 GATTCGTAGGTACAAAGCCCTACTCCAAAGCTGACGTTGAAGATTAAGAGAGACATGC 1020
Db 1040 GATTCGTAGGTACAAAGCCCTACTCCAAAGCTGACGTTGAAGATTAAGAGAGACATGC 1099
QY 1021 GTCCCTTTGAATAAAGGACGACACAAAGAAAGAGAGATCTTACCCAGCATATA 1080
Db 1100 GTCCCTTTGAATAAAGGACGACACAAAGAAAGAGAGATCTTACCCAGCATATA 1159
QY 1081 CCTGGGAGATGCTTCTCTCACTTCAATTTTACCTGCTGCTTGAATCCGAGCAATTCCT 1140
Db 1160 CCTGGGAGATGCTTCTCTCACTTCAATTTTACCTGCTGCTTGAATCCGAGCAATTCCT 1219
QY 1141 AAAAAGCATTTTGGCAGCCCTTGTGACTATACCAAGTGAAGTGAAGAGGCGAGG 1200
Db 1220 AAAAAGCATTTTGGCAGCCCTTGTGACTATACCAAGTGAAGTGAAGAGGCGAGG 1279
QY 1201 CTACAGAGAGCTGTGACAGTAAACAGAGGCGACCCGATTTATACCCGCTTTGTACGAGATGCC 1260
Db 1280 CTACAGAGAGCTGTGACAGTAAACAGAGGCGACCCGATTTATACCCGCTTTGTACGAGATGCC 1339
QY 1261 TGTGCTGCTGTTGGATCTCTCTGCTGCTTCCCTTTCGACGCCACCTAGTCTC 1320
Db 1340 TGTGCTGCTGTTGGATCTCTCTGCTGCTTCCCTTTCGACGCCACCTAGTCTC 1399
QY 1321 CTGCTCGAACAATCTCTAAACCTTCAACCCAGACCATATTTGCTGCAAGCTCAAGTTTA 1380
Db 1400 CTGCTCGAACAATCTCTAAACCTTCAACCCAGACCATATTTGCTGCAAGCTCAAGTTTA 1459
QY 1381 TTTCAACCCAGAAAGCTCCATTTTGTCTCAACATTTGGAATTTCTCTACTGCGACA 1440
Db 1460 TTTCAACCCAGAAAGCTCCATTTTGTCTCAACATTTGGAATTTCTCTACTGCGACA 1519
QY 1441 ACAGAGGTTCTGCGAAGGAGATATGTACAGGCTGCGGCTTGTGTTGCTTCACTT 1500
Db 1520 ACAGAGGTTCTGCGAAGGAGATATGTACAGGCTGCGGCTTGTGTTGCTTCACTT 1579

QY 1501 CTTACGCCAAACATATCATGATCCCATGAAAGACAGCGGAAAGCCCTGCTCTAAGATA 1560
Db 1580 CTTACGCCAAACATATCATGATCCCATGAAAGACAGCGGAAAGCCCTGCTCTAAGATA 1639
QY 1561 TCCATCTCTCTCGAACAACAATTTCTTCCATCTTACAGATGACCCCTCAATCCCATC 1620
Db 1640 TCCATCTCTCTCGAACAACAATTTCTTCCATCTTACAGATGACCCCTCAATCCCATC 1699
QY 1621 ATATGAGGAGTCCGAGAACCGGATACCCCGTTATTTGGTCTTCAACATAGAGAG 1680
Db 1700 ATATGAGGAGTCCGAGAACCGGATACCCCGTTATTTGGTCTTCAACATAGAGAG 1759
QY 1681 AAATCCCAAGAACACACCCAGATGGAATTTTGGAGCAATGTG--GTTTTTGGCTGC 1737
Db 1760 AAATCCCAAGAACACACCCAGATGGAATTTTGGAGCAATGTG--GTTTTTGGCTGC 1819
QY 1738 AGCATTAAGATAGGATTTATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGG 1797
Db 1820 AGCATTAAGATAGGATTTATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGG 1879
QY 1798 ATCTTAAGTCAATTAAGGTTTCTCTTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1857
Db 1880 ATCTTAAGTCAATTAAGGTTTCTCTTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1939
QY 1858 CCAGCAAGTATGTAACAAGACACATCCAGCTTCAAGGCTGAGAGGAGAGATCTCTC 1917
Db 1940 CCAGCAAGTATGTAACAAGACACATCCAGCTTCAAGGCTGAGAGGAGAGATCTCTC 1999
QY 1918 CTCAGAGAGAACGCCATATTTATGCTGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1977
Db 2000 CTCAGAGAGAACGCCATATTTATGCTGTGTGAGATGCAAAAGATATGCGCAAGATGTA 2059
QY 1978 CATGATGCCCTTGTGCAATATTAAGCAAGAGGTGAGTGAAGAACTGAAGCAATG 2037
Db 2060 CATGATGCCCTTGTGCAATATTAAGCAAGAGGTGAGTGAAGAACTGAAGCAATG 2119
QY 2038 AAAACCTGGCCACTTTAAAGAGAAAAACGCTACCTTCAGAGATTTTGTCTATAA 2094
Db 2120 AAAACCTGGCCACTTTAAAGAGAAAAACGCTACCTTCAGAGATTTTGTCTATAA 2176

RESULT 2
US-08-905-223-71
Sequence 71, Application US/08905223
Patent No. 622029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelien, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:


```

;
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 289..357
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 6.9
; OTHER INFORMATION: seq SLSLASHSVSC/SN
US-08-905-223-71

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Query Match      18.5%; Score 386.4; DB 4; Length 390;
Best Local Similarity 99.7%; Pred. No. 1,1e-117;
Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 968 AGGTACAAAGCCTACTCCAAAGACTGCAGCTTGAAGATAAAGAGAGACACTGCTCTTT 1027
DB 1 AAGTACAAAGCCTACTCCAAAGACTGCAGCTTGAAGATAAAGAGAGACACTGCTCTTT 60
QY 1028 TGAATAATAAGGACACACAAAGAAAGAGACTACCTTACCCAGCATATACCTGCGG 1087
DB 61 TGAATAATAAGGACACACAAAGAAAGAGACTACCTTACCCAGCATATACCTGCGG 120
QY 1088 GATGTTCTCTCCAGTTTCATTTTACCTGTGTCTTGAATCCGAGCAATTCCTAAAGAG 1147
DB 121 GATGTTCTCTCCAGTTTCATTTTACCTGTGTCTTGAATCCGAGCAATTCCTAAAGAG 180
QY 1148 CATTTTGGAGCCCTTGTGACTATACCACTGACAGTCTGCTGCTGCTGCTGCTGCTGCT 1207
DB 181 CATTTTGGAGCCCTTGTGACTATACCACTGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 1208 ACCTGTGCAGTAAACAAAGGGGACGCGATTATAGCCGCTTTGTAGAGATGCTGTGCT 1267
DB 241 ACCTGTGCAGTAAACAAAGGGGACGCGATTATAGCCGCTTTGTAGAGATGCTGTGCT 300
QY 1268 GCTTGTGATCTCCCTCGCTTCCCTTCCCTTGTGACAGCCACCACTCAGTCTCGCTCG 1327
DB 301 GCTTGTGATCTCCCTCGCTTCCCTTCCCTTGTGACAGCCACCACTCAGTCTCGCTCG 360
QY 1328 AACATCTTCTTAACCTCAACCCAGACC 1355
DB 361 AACATCTTCTTAACCTCAACCCAGACC 388

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RESULT 3
US-09-627-216A-13
; Sequence 13, Application US/09627216A
; Patent No. 6368837
; GENERAL INFORMATION:
; APPLICANT: Sarislan, Sima F
; APPLICANT: Tang, Xiao-Song
; APPLICANT: Q1, Wei Wei
; APPLICANT: Vannelli, Todd
; APPLICANT: Gatenby, Anthony
; TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
; FILE REFERENCE: BC1009 US NA
; CURRENT APPLICATION NUMBER: US/09/627,216A
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/147,719
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1863

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; TYPE: DNA
; ORGANISM: Helianthus tuberosus
US-09-627-216A-13

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Query Match      2.8%; Score 58.2; DB 4; Length 1863;
Best Local Similarity 49.3%; Pred. No. 1,3e-08;
Matches 255; Conservative 0; Mismatches 238; Indels 24; Gaps 3;

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QY 1576 ACAACAATTTCTTCCACTTACCATAGATAGCCCCCTCAATCCCATATATGTTGGTCA 1635
DB 1276 AGACATGCACTTACCATAGATAGCCCCCTCAATCCCATATATGTTGGTCA 1335
QY 1636 GGAACCGGATAGCCCGTTTATGCTTCTTACCAATAGAGAACTCCAGAACAA 1695
DB 1336 GGAACCGGATAGCCCGTTTATGCTTCTTACCAATAGAGAACTCCAGAACAA 1395
QY 1696 CACCCAGATGAAATTTTGGACCAATTTGCTTTTGGCTGACGACATAGATAGGAT 1755
DB 1396 GGAACCGA---ACTCGGTCATTCATTTTGTCTTGGTTCGGAACCGTAAAGTGAT 1452
QY 1756 TATCATATGCAAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATCAAG 1815
DB 1453 TTCAATATATGCAAAATGACATGACACACTTTTGAATAAGGCGCTTTCCAGCTTGC 1512
QY 1816 GTTTCCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAAAGCCCAAGATATGACAA 1875
DB 1512 ATGCTTCTCTCGC-----GAAAGGCGCATCTTAAGAAATACGTGCA 1554
QY 1876 GACACATTCACCTTCATGCGCCAGACAGTGGGAGAGATCTCTCCAGAGAACGCCAT 1935
DB 1555 CATAAATATGACCAAAAGCCTTCGATAT---ATGAAACATCTTCTGAGGAGCATAC 1611
QY 1936 ATTTATGTTGTTGAGATGCAAAAGATATGAGCAAGATGTACATGATCCCTTGCA 1995
DB 1612 TTATAGTGTGTGATGATCCAAAGCATGCTTAAGATGTACACCAAGCCCTTACACC 1671
QY 1996 ATAAATAGCAAGAGTTGAGTGTGAATAAGCAAGCAATGAACCCCTGCGCATTTA 2055
DB 1672 ATTTGCAAGAACAGGAATTTGATCTCTCTTAAGCAAGACCTGTATGTGAAGATCA 1731
QY 2056 AAGAGAAAGAAAGCCTTACCTTCAAGATTTTGTGCT 2092
DB 1732 CAAATGTCGGAAGATACCTCGTATGTTGTGAT 1768

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RESULT 4
US-08-365-486A-18
; Sequence 18, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 31.
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.

```

```

? REGISTRATION NUMBER: 38,615
? REFERENCE/DOCKET NUMBER: 8255-0018
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 324-0880
? TELEFAX: (415) 324-0960
? INFORMATION FOR SEQ ID NO: 18:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4353 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al,
? INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..4305
US-08-365-486A-18

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QY	1888	CTTCATGCGCCAGCAGGTGGGCGAGAACTCCTCTCCAGGAGAAAGCCCATATTTATGTGAGT	1947
Db	4000	GAGCAGCTGGCGGAGAGTCTGTGTACCGAGCCCTGAAGGAGCAAGGGGGCCACATATTACGTC	4059
QY	1948	GGAGATCCAAAGATATATGGCCAAAGATATACATGATGCCCTTGTGCAAAATTAATAAGCAA	20072
Db	4060	TGTGGGAGCGACACCATGTGGTGTGTGATGTCTCTCAAGGCATTCAGCGGATCATGACCCAG	4119
QY	2008	GAGGTTGGAGTTGAAAAACTAGAAAGCAATCAAAACCCTGGCCACTTTAAAAAGAGAAAA	2067
Db	4120	CAGGGGAAGCTCTTCGGCAGAGGAGCGCGGCGTATTTCATCACCCGATGAGGAGATGACAAAC	4179
QY	2068	CGTACCTTCAGATATTTT	2086
Db	4180	CGATACCATGAGATATTTT	4198

RESULT 6
US-08-365-486A-20
; Sequence 20, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:

1
2 APPLICANT: Bishopric, Nanette H.
3 TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
4 TITLE OF INVENTION: Therapeutic Constructs
5
6 NUMBER OF SEQUENCES: 31
7
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Dehlinger & Associates
10 STREET: 350 Cambridge Avenue, Suite 250
11 CITY: Palo Alto
12 STATE: CA
13 COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994

ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:

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: INFORMATION FOR SEQ ID NO: 20
:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 4780 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: double
:   TOPOLOGY: linear
:   MOLECULE TYPE: cDNA to mRNA
:   HYPOTHETICAL: NO

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: ANTI-SENSE: NO
: ORIGINAL SOURCE: Human NOS-3N gene, Nakane, et al
: INDIVIDUAL ISOLATE:
: INDIVIDUAL ISOLATE: FEBS Lett 316:175 (1993)

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; NAME/KEY: CDS
; LOCATION: 431..4732
US-08-365-486A-20

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Query Match 2.78; Score 57.4; DB 2; Length 4780;

Matches 233; Conservative 0; Mismatches 251; Indels 15; Gaps 1;

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Db	4142	TTCCACCTGCCCGGAACCCCCCAAGTCCCTGCATCTCTGTTGGACCAAGGACCGGCATT	4201
OY	1548	GCCCCCTTTATTGGGCTCTTCAACCATTAAGAGAACTCCAAAGAACCCCGATGGA	1707
Db	4202	GCCCCCTTTCCGAACCTTCTGGCAACACACGGCAATTTGATATCCAAACCAAGGAATGAAC	4261
OY	1708	AATTTTGGAGCAATGTGGTTTTTGGCTGCAGGCATTAAGATTAAGGATTAATCTAATTCAGA	1767
Db	4262	CCCTGCCCCCATNGTCTCGTCTTGTTGGGGCCGGCAATCCAAAGATTAAGTATCTACAGG	4321
OY	1768	AAAGAGCTCAGACATTTTCTTTAAGCATGGATCTTAACTCACTCAAAAGTTTCTTCTCA	1827
Db	4322	GAAGAGACCTTCGACGGGCCAAGAACAAAGGGGCTCTTCAGAGAGCTACACGGCTTACTCC	4381
OY	1828	AGAGATGCTCTGTTGGGGAGGAGGAAGCCCCACCAAAAGTATGTATCAAGAACATATCCAG	1887
Db	4382	C-----GGAGCCAGACAAACCAAGAAAGTACGTGACAGACATCTCTGCAG	4426
OY	1888	CTTCATGGCCAGAGTGGCCGAGATCCTCTCCAGAGGAAGCGCCATATTTATGTGTGT	1947
Db	4427	GAGCAGCTGGCGGAGTCTGTACCGAGCCCTGAAGGAGCAAGGGGGCCACATATACGTC	4486
OY	1948	GGAACATCGAAGAATATGGCCAAAGATGTACATATGCGCTTGTGGCAATATTAAGCAA	2007
Db	4487	TGTGGGGACGTCCACCATGTGCTGTGATGTCTCTCAAGGCATTCACGCGCATATACCCAG	4546
OY	2008	GAGGTTGGAGTGTGAANAACCTAGAAGCATGAANAACCCGTGCCACATTTTAAAGAAGAAAA	2067
Db	4547	CAGGGAAGCTCTCGGCGAGAGGACGCGGGCTATTATCATCAGCCGATGAGGGATGACAAAC	4606
OY	2068	CGTACCTTCCAGATATTT	2086
Db	4607	CGATACCATGAGATATTT	4625

RESULT 7
US-09-123-708-3
; Sequence 3, Application US/09123708

* APPLICANT: SCHRAEDER, Juergen
* APPLICANT: GOEDECKE, Axel
* TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
* TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
* FILE REFERENCE: 511169-2003
* CURRENT APPLICATION NUMBER: US/09/123,708
* CURRENT FILING DATE: 1998-07-28
* EARLIER APPLICATION NUMBER: 08/553,503
* EARLIER FILING DATE: 1996-03-01
* EARLIER APPLICATION NUMBER: P4411402.8
* EARLIER FILING DATE: 1994-03-31
* NUMBER OF SEQ ID NOS: 6

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; EARLIER FILING DATE: 1994-03-31
; * NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4780
; TYPE: DNA
; ORGANISM: Cytomegalovirus
US-09-123-708-3

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Query Match	2.78;	Score 57.4;	DB 3;	Length 4780;
Best Local Similarity	46.78;	Pred. No. 4.7e-08;		
Matches 233; Conservative	0;	Mismatches 251;	Indels 15	

QY	1588	TTCCACTTACCAGAT
Db	4142	TTCCACCTGCCCCGC

1648 GCCCGTTTATTGGGTTCTACACATAGAGAGAACTCCAAGAACACACCCAGATGGA 1707

Db 4202 GCCCCTTCCGAAGCTTCTGGCAACAGCGCAATTGATATCCACACAAGGAATGAAC 4261

Qy 1708 AATTTTGGACAA1GTGCTTTTTPPGCGTCAGCGCATTAAGATAGGATATCATTTCCAGA 1767

FEATURE:
NAME/KEY: CDS
LOCATION: 431..4732
US-08-880-342-20

Query Match 2.7%; Score 57.4; DB 4; Length 4780;
Best Local Similarity 46.7%; Pred. No. 4.7e-08;
Matches 233; Conservative 0; Mismatches 251; Indels 15; Gaps 1;

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OY 1588 TTCACCTTACAGATGACCCCTCATCCCATCATATGATGGTGGTCCAGAACCGGCATTA 1647
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DB 4142 TTCACCTGCCCCGAGACCCCAAGTCCCTGATCTCTGTGGACAGCGCCGANT 4201
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OY 1648 GCCCCGTTTATGAGTCTCTACATAGAGAACTCAAGAACACACCCAGATGGA 1707
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DB 4202 GCCCCGTTTCCAGAGTTCTGGCAACAGGGCATTTGATATCCACACAAAGATGAA 4261
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OY 1708 AATTTGAGACAAATGTGTTTTTGGCTGCAGGCATTAAGATAGGATTAATCTATTCAGA 1767
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4262 CCCTGCCCATGATCTCTGTTCTGGGTCCGGCAATCCAGATGATCATATCTACAGG 4321
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1768 AAGAGCTACAGCATTTCTTAAGCATGAGATCTTAAGTCTTAAGGTTCTCTCA 1827
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4322 GAGAGACCTTCAGAGCCCAAGACAAAGGGGCTTTCAGAGAGCTGTACACGGCTTACTCC 4381
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OY 1828 AGAGATGCTCTGTTGGGAGAGAGAGCCCGCAGCAAGTATGACAAACACATCCAG 1887
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DB 4382 C-----GGGAGCCAGACAAACCAAGAGTACGTGACAGACATCTCTGACAG 4426
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OY 1888 CTTACATGCCCAGACAGTGGCGCAATCTCTCCAGAGAACCGCCATATTTATGTGT 1947
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DB 4427 GAGCAGCTGGGGAGTCTGTGTACCGAGCCCTGAAGAGCAAGGGGGCCACATATACGTC 4486
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OY 1948 GGAGATGCAAGAAATATGCGCAAGATGTACATGATGCCCTTGTCAAAATATATAGCAAA 2007
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DB 4487 TGTGGGAGACGTACCATGTGCTGTATGTCTCAAAAGCATTCAGCGCATCTGACCCAG 4546
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OY 2008 GAGGTTGAGTTGAAAACTAGAACCAATGAACCCCTGGCCACTTTAAAGAGAAAAA 2067
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DB 4547 CAGGGGAAGCTCTCGGACAGAGACGCCGGCTATTATCATCAGCCGATGAGGATGACAA 4606
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OY 2068 CGCTACCTTCAGATATTT 2086
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DB 4607 CGATACCATGAGATATTT 4625
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RESULT 10

US-08-365-486A-12
Sequence 12, Application US/08365486A
Patent No. 5834306

GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: rat bnos cDNA

Query Match 2.5%; Score 52.6; DB 2; Length 5057;
Best Local Similarity 46.1%; Pred. No. 1.9e-06;
Matches 230; Conservative 0; Mismatches 254; Indels 15; Gaps 1;

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OY 1588 TTCACCTTACAGATGACCCCTCATCCCATCATATGATGGTGGTCCAGAACCGGCATTA 1647
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OY 1648 GCCCCGTTTATGAGTCTCTACATAGAGAACTCAAGAACACACCCAGATGGA 1707
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DB 4108 GCACCTTCCGAAGCTTCTGGCAACAGCGACAAATTTGACATCCACACAAAGATGAA 4167
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OY 1708 AATTTGAGCAATGTGTTTTTGGCTGCAGGCATTAAGATAGGATTAATCTATTCAGA 1767
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DB 4168 CGGTGCCCATGATGTTCTGTGTGCTGGGTGCACAATCCAAATGATCATATCTACAGA 4227
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OY 1768 AAGAGCTACAGCATTTCTTAAGCATGAGATCTTAAGTCTTAAGGTTCTCTCA 1827
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DB 4228 GAGGAGACCTTCAGAGCTTAAGAACAGGGCGTCTTCAGAGACTGTACACTGCTTATTC 4287
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OY 1888 CTTACATGCCCAGACAGTGGCGGAATCTCTCTCCAGAGAACGCCATATTTATGTGT 1947
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DB 4333 GAACAGCTGGCTGTGTGTGTACCGCGCCCTGAAGAGACAGAGGCCCATTTATGTC 4392
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OY 1948 GGAGATGCAAGAAATATGCGCAAGATGTACATGATGCCCTTGTCAAAATATATAGCAAA 2007
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DB 4393 TGTGGGAGACGTACCATGTGCGCCCGATGTCTCAAAAGCATTCAGCGCATTAAGACCCAG 4452
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OY 2008 GAGGTTGAGTTGAAAACTAGAACCAATGAACCCCTGGCCACTTTAAAGAGAAAAA 2067
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DB 4453 CAGGGGAAGCTCTCGAGAGAGACCGTGTGTATTCATCAGAGGCTGAGGATGACAA 4512
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OY 2068 CGCTACCTTCAGATATTT 2086
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DB 4513 CGTACCATGAGACATCT 4531
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RESULT 11

US-08-880-342-12
Sequence 12, Application US/08880342
Patent No. 6218179

GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

1 TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
2
3 TITLE OF INVENTION: Therapeutic Constructs
4
5 NUMBER OF SEQUENCES: 37
6
7 CORRESPONDENCE ADDRESS:
8
9 ADDRESSEE: Dehlinger & Associates
10
11 STREET: 350 Cambridge Avenue, Suite 250
12
13 CITY: Palo Alto
14
15 STATE: CA
16
17 COUNTRY: USA
18
19 ZIP: 94306
20
21 COMPUTER READABLE FORM:
22
23 MEDIUM TYPE: Floppy disk
24
25 COMPUTER: IBM PC compatible
26
27 OPERATING SYSTEM: PC-DOS/MS-DOS
28
29 SOFTWARE: PatentIn Release #1.0, Version #1.25
30
31 CURRENT APPLICATION DATA:
32
33 APPLICATION NUMBER: US/08/880,342
34
35 FILING DATE: 23-JUN-1997
36
37 CLASSIFICATION: 514
38
39 PRIOR APPLICATION DATA:
40
41 APPLICATION NUMBER: PCT/IB95/00996
42
43 FILING DATE: 13-NOV-1995
44
45 PRIOR APPLICATION DATA:
46
47 APPLICATION NUMBER: US 08/365,486
48
49 FILING DATE: 23-DEC-1994
50
51 ATTORNEY/AGENT INFORMATION:
52
53 NAME: Sholtz, Charles K.
54
55 REGISTRATION NUMBER: 38,615
56
57 REFERENCE/DOCKET NUMBER: 8255-0018.30
58
59 TELECOMMUNICATION INFORMATION:
60
61 TELEPHONE: (415) 324-0880
62
63 TELEFAX: (415) 324-0960
64
65 INFORMATION FOR SEQ ID NO: 12:
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67 SEQUENCE CHARACTERISTICS:
68
69 LENGTH: 5057 base pairs
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71 TYPE: nucleic acid
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73 STRANDEDNESS: double
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75 TOPOLOGY: linear
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77 MOLECULE TYPE: cDNA to mRNA
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79 HYPOTHETICAL: NO
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81 ANTI-SENSE: NO
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83 ORIGINAL SOURCE:
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85 INDIVIDUAL ISOLATE: rat bnos cDNA
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87 FEATURE:
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89 NAME/KEY: CDS
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91 LOCATION: 349..4638
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93 US-08-880-342-12
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[illegible]

RESULT 13
 US-08-936-165A-113
 : Sequence 113, Application US/08936165A
 : Patent No. 6348582
 : GENERAL INFORMATION:
 : APPLICANT: Black, Michael
 : APPLICANT: Burnham, Martin
 : APPLICANT: Hodgson, John
 : APPLICANT: Knowles, David
 : APPLICANT: Lonetto, Michael
 : APPLICANT: Nicholas, Richard
 : APPLICANT: Pratt, Julie
 : APPLICANT: Reichard, Richard
 : APPLICANT: Rosenberg, Martin
 : APPLICANT: Ward, Judith
 : TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
 : TITLE OF INVENTION: Polypeptides and Their uses
 : NUMBER OF SEQUENCES: 534
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: SmithKline Beecham Corporation
 : STREET: 709 Swedeland Road
 : CITY: King of Prussia
 : STATE: PA
 : COUNTRY: USA
 : ZIP: 19406-0939
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/936,165A
 : FILING DATE: 24-SEP-1997
 : CLASSIFICATION: 536
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/027,032

```

1      FILING DATE: 24-SEP-1996
2      ATTORNEY/AGENT INFORMATION:
3      NAME: Gimmil, Edward R
4      REGISTRATION NUMBER: 38,891
5      REFERENCE/DOCKET NUMBER: P50549
6      TELECOMMUNICATION INFORMATION:
7      TELEPHONE: 610-270-4478
8      TELEFAX: 610-270-5090
9      TELEX:
10     INFORMATION FOR SEQ ID NO: 113:
11     SEQUENCE CHARACTERISTICS:
12     LENGTH: 1448 base pairs
13     TYPE: nucleic acid
14     STRANDEDNESS: single
15     TOPOLOGY: linear
16     MOLECULE TYPE: Genomic DNA
17     US-08-936-165A-113

```

Query Match	2.48;	Score 50.2;	DB 4;	Length 1448;
Best Local Similarity	58.38;	Pred. No. 5e-06;		
Matches 88; Conservative	0;	Mismatches 63;	Indels 0;	Gaps 0;

QY	1936	ATTATATGCTGTGGAGATGCAAAAGAAATPYGGCCAAAGATGATCAATGATGACCTTGTGCAA	1995
QY	116	ATCTATATTTGTGGCGATGAAAATAATGTATGGCGAAAGATGTCCATCAAGCCATTAAAGAT	175
QY	1996	ATATTAACGAAGAAGGTGGAGCTTGAAATACTAGAAAGCAATGAAGAAACCCCTGGCCACTTAA	205
Db	176	GTATTTGGTAAAGAACGTCATATTTCTCTACAGACAGACAGAGTTATTTATTGGACCAAAATG	235
QY	2056	AAAGAGAAAAACGCTACCTTCAGATATTTT	2086
Db	236	AAACACACAAACGCTATCAACGATGATTTT	266

```

RESULT 14
US-09-134-001C-1557
: Sequence 1557, Application US/09134001C
: Patent No. 6380370
: GENERAL INFORMATION:
: APPLICANT: Lynn Doucette-Stamm et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
: TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: GTC-007
: CURRENT APPLICATION NUMBER: US/09/134,001C
: PRIOR FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: US 60/064,964
: PRIOR FILING DATE: 1997-11-08
: PRIOR APPLICATION NUMBER: US 60/055,779
: PRIOR FILING DATE: 1997-08-14
: NUMBER OF SEQ ID NOS: 5674
: SEQ ID NO 1557
: LENGTH: 1890
: TYPE: DNA
: ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1557

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[illegible]

QY 1734 CTGACGAGCATAGATAGGATTTATCTATTTCAGAAAAGCTCAGACATTTCTTAAACA 1793
Db 1554 AGATCAACACTTCTACTACAGATTTCTGTATCAAAACGGAATGCGAAGATGGCTTGAGA 1613
QY 1794 TGGGATTTACTCATCTAAGGTTTCTCTCAAGAGATGCTCCTGTTGGGAGAGAGA 1853
Db 1614 TGGAACTTATCAATAATAGATGCTTTCTCTAGAGA--TACTGATTAATAAAGTGTA 1670
QY 1854 AGCCGACCAAGATATGATACAGACATCCAGCTTCATGCGCAGCAGGTTGGCAGAT 1913
Db 1671 TGTGACACATAAATTTGTAAGAAATAGTACACATTTAATCATG----- 1716
QY 1914 CCTCTCAGAGAAAGCGCCATATTATGTGTGTGAGATGCAAGAAATATGCCAAGA 1973
Db 1717 ---ATTGAAATGCGCTACTATTATGTATGTGTGATGAAAGTAAATGCAAGA 1772
QY 1974 TGTACATATATGCTTGTGCAAAATATAAGCAAAAGGTGAGTTGAAAACTGAAAC 2033
Db 1773 TGTATCAAGCATTAATAAATGTGTATCAAAAGCAAAACCTATCTGAAACAGATGC 1832
QY 2034 AATGAAACCTGCGCCTTTAAAGAAAGAAAAAGCTACC 2074
Db 1833 AGAAGATACTTAAACAAATGAAAGATTAAGATATC 1873

RESULT 15
US-08-232-463-14; Sequence 14, Application US/08232463
; Patent No. 5670367

GENERAL INFORMATION:

; APPLICANT: DORNER, F.
; APPLICANT: SCHEFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232.463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935.313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29, 768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: PT29pt-F15

; US-08-232-463-14

Query Match 2.2%; Score 46.2; DB 1; Length 7218;
Best Local Similarity 3.8%; Pred. No. 0.00032;
Matches 15; Conservative 217; Mismatches 165; Indels 0; Gaps 0;

QY 1227 GGCAGCCGATTTATGCGCTTGTGTAGAGATGCTGTGCTGCTGTTGATGCTCTCT 1286
Db 1041 GCGTCAGAGTGCAGGAGCTTGCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1100
QY 1287 CGCTTCCCTTCTTGCAGCCACACCTCAGTCTCTGCTGCAACATCTTCTTAACCTCA 1346
Db 1101 TT 1160
QY 1347 ACCGAGCCATATGCTGTGCAAGCTCAAGTTTATTTACCGAGAAAGCTCATTTGT 1406
Db 1161 TT 1220
QY 1407 CTTCACATTTGTGAATTTCTGTCTAGTCCCAACAGAGTTCTGCGAAGGAGTATG 1466
Db 1221 TT 1280
QY 1467 TACAGGCTGCGCTGCTGTGTGCTTCACTTCTTCAAGCAACATACATGCCA 1526
Db 1281 TT 1340
QY 1527 TGAAGACAGCGGAAAGCCCTGCTCTAAGATATCATCTCTCGAACAACAATTG 1586
Db 1341 TT 1400
QY 1587 TTTCACCTTACCAATGACCCCTCATGCCATCATCA 1623
Db 1401 TT 1437

Search completed: July 29, 2003, 13:07:21
Job time : 90.9321 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 29, 2003, 09:58:39 ; Search time 88.8896 Seconds
(without alignments)
7221.032 Million cell updates/sec

Title: US-09-371-347a-47

Perfect score: 2093

Sequence: 1 atgagagaggttcctgtact.....cttcagatatctgtcatcaaa 2093

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

- 1: /cgn2_6/prodata/1/lna/5A_COMB.seq:*
- 2: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
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- 4: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
- 5: /cgn2_6/prodata/1/lna/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2079	99.3	3259	4	US-09-318-448-23
2	386.4	18.5	350	4	US-08-905-223-71
3	64.6	3.1	4353	2	US-08-365-486A-18
4	64.6	3.1	4353	4	US-08-880-342-18
5	64.6	3.1	4780	2	US-08-365-486A-20
6	64.6	3.1	4780	3	US-09-123-708-3
7	64.6	3.1	4780	3	US-09-123-624-3
8	64.6	3.1	4780	4	US-08-880-342-20
9	59.8	2.9	5057	4	US-08-365-486A-12
10	59.8	2.9	5057	2	US-08-880-342-12
11	59.8	2.9	5108	1	US-07-642-002-1
12	56	2.7	1863	4	US-09-627-216A-13
13	55.2	2.6	1890	4	US-09-134-001C-1357
14	50.2	2.4	1448	4	US-08-936-165A-113
15	48.4	2.3	4145	4	US-09-302-620B-82
16	46.8	2.2	4206	4	US-09-302-620B-81
17	46.2	2.2	7218	1	US-08-232-653-14
18	44	2.1	307	4	US-09-172-711-24
19	43.4	2.1	7218	4	US-08-232-653-14
20	40.6	1.9	382	4	US-08-976-259-78
21	40.6	1.9	4041	1	US-08-147-812-4
22	40.6	1.9	4110	3	US-09-123-708-1
23	40.6	1.9	4110	3	US-09-123-624-1
24	40.6	1.9	4155	1	US-08-147-812-6
25	36.6	1.7	3701	1	US-08-553-279-1
26	36.6	1.7	45346	4	US-09-146-053-6
27	36	1.7	4089	1	US-07-908-245-1

28	36	1.7	4097	3	US-09-123-708-5	Sequence 5, App11
29	36	1.7	4097	3	US-09-123-624-5	Sequence 5, App11
30	35.4	1.7	1296	4	US-09-134-001C-1501	Sequence 1501, App
31	34.2	1.6	1569	1	US-08-680-726A-57	Sequence 57, App1
32	34.2	1.6	1569	3	US-09-092-409-57	Sequence 57, App1
33	34.2	1.6	10592	1	US-08-680-726A-51	Sequence 51, App1
34	34.2	1.6	10592	1	US-08-680-726A-52	Sequence 52, App1
35	34.2	1.6	10592	3	US-09-092-409-51	Sequence 51, App1
36	34.2	1.6	10592	3	US-09-092-409-52	Sequence 52, App1
37	34	1.6	2223	1	US-08-257-073-4	Sequence 4, App11
38	33.8	1.6	1702	1	US-08-261-822A-14	Sequence 14, App1
39	33.8	1.6	1702	5	PCT-US95-07744A-14	Sequence 14, App1
40	33.8	1.6	4146	1	US-08-261-822A-15	Sequence 15, App1
41	33.8	1.6	4146	5	PCT-US95-07744A-15	Sequence 15, App1
42	33.4	1.6	2193	4	US-09-427-261-2	Sequence 2, App11
43	33.4	1.6	2193	4	US-09-427-261-3	Sequence 3, App11
44	33.2	1.6	2277	1	US-08-676-967-2	Sequence 2, App11
45	33.2	1.6	2277	1	US-08-676-974-2	Sequence 2, App11

ALIGNMENTS

RESULT 1
US-09-318-448-23
; Sequence 23, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Sternoos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 3259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-23

Query Match 99.3%; Score 2079; DB 4; Length 3259;
Best Local Similarity 99.8%; Pred. NO. 0;
Matches 2093; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY	1	ATGAGAGAGTTTCTGTTACTATATGCTACACAGAGGAGGCAAGCCATCGCAGAA	60
DB	80	ATGAGAGAGTTTCTGTTACTATATGCTACACAGAGGAGGCAAGCCATCGCAGAA	139
QY	61	GAATGTGTAGCAAGCTGTGTACATGATTTTCTGACATCTTCACTGATTAGTGA	120
DB	140	GAATGTGTAGCAAGCTGTGTACATGATTTTCTGACATCTTCACTGATTAGTGA	199
QY	121	TCGATATGATGATGCTTAAACCGAAGCTCTGTTGTTGGTTTACACAG	180
DB	200	TCGATATGATGATGCTTAAACCGAAGCTCTGTTGTTGGTTTACACAG	259
QY	181	GGCAGCAGAGACCCAGCCGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCA	240
DB	260	GGCAGCAGAGACCCAGCCGACACAGCCGCAAGTTTGTAAAGAAATACAGAACCA	319
QY	241	CTGCGGCTGATTTCTTGTCTACCTCGGCTATGGTTACTGGTCTCGGTTATTCGA	300
DB	320	CTGCGGCTGATTTCTTGTCTACCTCGGCTATGGTTACTGGTCTCGGTTATTCGA	379
QY	301	TACACCTACTTTTGCATGGGGGAGATTAATGATTAAGACATTCAGAGCTTGAGCC	360
DB	380	TACACCTACTTTTGCATGGGGGAGATTAATGATTAAGACATTCAGAGCTTGAGCC	439
QY	361	CGGCAATTTCTATGACATGACATGACATGCTGTAGATTAGAACTTGTGTTGAG	420

Db 440 CGCATTCTGATGACACTGACATGACATGATGCTGTAGGTTTGAACATTTGGTTGAG 499
 QY 421 CCGTGATGCTGACTCTGGCCAGCCCTCAGAAAGCATTTTAGTCAAGCAGAGCAAA 480
 Db 500 CCGTGATGCTGACTCTGGCCAGCCCTCAGAAAGCATTTTAGTCAAGCAGAGCAAA 559
 QY 481 GAGAGATTAAGTGGCGACTCCGGGTGACATCCTGATCTGTTGAGAGACAGCCTTGTG 540
 Db 560 GAGAGATTAAGTGGCGACTCCGGGTGACATCCTGATCTGTTGAGAGACAGCCTTGTG 619
 QY 541 AAGCAGAGCTGCTACATGTAATCTCAAGTGCAGCTTGTGAGATTCGATGATTCAGA 600
 Db 620 AAGCAGAGCTGCTACATGTAATCTCAAGTGCAGCTTGTGAGATTCGATGATTCAGA 679
 QY 601 AGAAGGATTCGAGGTTTGAAGCAAAATGACGTGAACAGCAACCAATCAATGTTGTA 660
 Db 680 AGAAGGATTCGAGGTTTGAAGCAAAATGACGTGAACAGCAACCAATCAATGTTGTA 739
 QY 661 ATTGAAGATTTGAGTCTCATTACCCGTTGCGTACCCCACTCTGACAAAGCCTCTG 720
 Db 740 ATTGAAGATTTGAGTCTCATTACCCGTTGCGTACCCCACTCTGACAAAGCCTCTG 799
 QY 721 AATATTCGTTTACCCCAAGATATTTACAGTACATGTCAGAGAGTCTCTGGCCAG 780
 Db 800 AATATTCGTTTACCCCAAGATATTTACAGTACATGTCAGAGAGTCTCTGGCCAG 859
 QY 781 GAGGAAAGCCAGATATCTGACTTCAAGATCCAGATCTTTTCAAGTGCATTTCAAG 840
 Db 860 GAGGAAAGCCAGATATCTGACTTCAAGATCCAGATCTTTTCAAGTGCATTTCAAG 919
 QY 841 GCAGTTCACTTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 Db 920 GCAGTTCACTTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 979
 QY 901 TCAAAATCAGACTTTTCTCAGCTGAGATGATGATGATGATGATGATGATGATGAT 960
 Db 980 TCAAAATCAGACTTTTCTCAGCTGAGATGATGATGATGATGATGATGATGATGAT 1039
 QY 961 GATTTCTGAGTACAAAGCCTTCTCAAGATGATGATGATGATGATGATGATGATGAT 1020
 Db 1040 GATTTCTGAGTACAAAGCCTTCTCAAGATGATGATGATGATGATGATGATGATGAT 1099
 QY 1021 GTCTTTTGAATAAAGGACAGACAAAGAAAGAGAGTACCTTACCCAGCATATA 1080
 Db 1100 GTCTTTTGAATAAAGGACAGACAAAGAAAGAGAGTACCTTACCCAGCATATA 1159
 QY 1081 CTTGCGGAGTCTCTCCAGTTCAATTTTACCGTGTGTTGAATCCGAGCAATTCCT 1140
 Db 1160 CTTGCGGAGTCTCTCCAGTTCAATTTTACCGTGTGTTGAATCCGAGCAATTCCT 1219
 QY 1141 AAAAAGCATTTTGGAGCCCTTGTGACTATACAGTACAGTGTGTAAGAGCGAG 1200
 Db 1220 AAAAAGCATTTTGGAGCCCTTGTGACTATACAGTACAGTGTGTAAGAGCGAG 1279
 QY 1201 CTACAGAGAGTGTGAGTAAACAAGGGGAGCCGATTAATAGCCGCTTTTGAAGATGCC 1260
 Db 1280 CTACAGAGAGTGTGAGTAAACAAGGGGAGCCGATTAATAGCCGCTTTTGAAGATGCC 1339
 QY 1261 TGTGCTGCTGTGATCTCTCCAGCTTCTCCGTTCCCTTCCGAGCCAGCAGCAGCTC 1320
 Db 1340 TGTGCTGCTGTGATCTCTCCAGCTTCTCCGTTCCCTTCCGAGCCAGCAGCAGCTC 1399
 QY 1321 CTGCTGCAACATCTTCTTAACCTCAACCCAGACCAATATTCGTGTGCAAGCTCAAGTTTA 1380
 Db 1400 CTGCTGCAACATCTTCTTAACCTCAACCCAGACCAATATTCGTGTGCAAGCTCAAGTTTA 1459
 QY 1381 TTTTACCCAGAAAGCTCCATTTTGTCTCAACATTTTGAATTTTGTCTACTGCCACA 1440
 Db 1460 TTTTACCCAGAAAGCTCCATTTTGTCTCAACATTTTGAATTTTGTCTACTGCCACA 1519
 QY 1441 ACAGAGTCTGCGGAAGGAGATATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 Db 1520 ACAGAGTCTGCGGAAGGAGATATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1579

QY 1501 CTTGAGCCAAACATACATGATCCCATGAAGACAGCGGAAAGCCCTGGCTCCTAAGATA 1560
 Db 1580 CTTGAGCCAAACATACATGATCCCATGAAGACAGCGGAAAGCCCTGGCTCCTAAGATA 1639
 QY 1561 TCCATCTCTCTGGAACAAATTTCTTCCACTTACCAAGTGAACCCCTCAATCCCATC 1620
 Db 1640 TCCATCTCTCTGGAACAAATTTCTTCCACTTACCAAGTGAACCCCTCAATCCCATC 1699
 QY 1621 ATATGCTGCTGGAACAAAGCCGATGAGCCCTGTTTGTGTTTCTTCAACAT ---AG 1676
 Db 1700 ATATGCTGCTGGAACAAAGCCGATGAGCCCTGTTTGTGTTTCTTCAACATAGAGAG 1759
 QY 1677 AAATCCAAAGAACACACCCAGATGAATTTTGGACCAATGCTGTTTGTGCTGC 1736
 Db 1760 AAATCCAAAGAACACACCCAGATGAATTTTGGACCAATGCTGTTTGTGCTGC 1819
 QY 1737 AGGCATAGGATAGGATATATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGG 1796
 Db 1820 AGGCATAGGATAGGATATATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGG 1879
 QY 1797 ATCTTACTCATCTAAAGGTTTCTTCTCAAGAGATCTCTGTTGGGAGAGAGAGCC 1856
 Db 1880 ATCTTACTCATCTAAAGGTTTCTTCTCAAGAGATCTCTGTTGGGAGAGAGAGCC 1939
 QY 1857 CCAGCAAGATATGATACAAAGACATCCAGCTTCTGAGAGAGTGGGAGAGATCTC 1916
 Db 1940 CCAGCAAGATATGATACAAAGACATCCAGCTTCTGAGAGAGTGGGAGAGATCTC 1999
 QY 1917 CTCAGAGAGAGCGGCATATTTATGTGTGTGAGAGTCAAGAAATATGAGCAAGATGTA 1976
 Db 2000 CTCAGAGAGAGCGGCATATTTATGTGTGTGAGAGTCAAGAAATATGAGCAAGATGTA 2059
 QY 1977 CATGATGCTCTTGTGCAATTAATATGCAAGAGTGTGAGATTTGAAACATGAGAGCATG 2036
 Db 2060 CATGATGCTCTTGTGCAATTAATATGCAAGAGTGTGAGATTTGAAACATGAGAGCATG 2119
 QY 2037 AAAACCTGGCCACTTTAAAGAAAGAAAGCGTACCTTGAGATATTTGGTCAATA 2093
 Db 2120 AAAACCTGGCCACTTTAAAGAAAGAAAGCGTACCTTGAGATATTTGGTCAATA 2176

RESULT 2
 US-08-905-223-71
 : Sequence 71, Application US/08905223
 : Patent No. 6222029
 : GENERAL INFORMATION:
 : APPLICANT: Edwards, Jean-Baptiste D.
 : APPLICANT: Duclert, Aymeric
 : APPLICANT: Lacroix, Bruno
 : TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
 : NUMBER OF SEQUENCES: 503
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Knobbe, Martens, Olson & Bear
 : STREET: 501 West Broadway
 : CITY: San Diego
 : STATE: California
 : COUNTRY: USA
 : ZIP: 92101-3505
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy Disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: Win95
 : SOFTWARE: Word
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/905,223
 : FILING DATE:
 : CLASSIFICATION: 536
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Israel, Ned A.
 : REGISTRATION NUMBER: 29,655
 : REFERENCE/DOCKET NUMBER:
 : TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: DOUBLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: CDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo Sapiens
 TISSUE TYPE: Brain
 FEATURE:
 NAME/KEY: sig-peptide
 LOCATION: 289..357
 IDENTIFICATION METHOD: Von Heijne matrix
 OTHER INFORMATION: score 6.9
 OTHER INFORMATION: seq SLSLASHSVSC/SN
 US-08-905-223-71

Query Match 18.5%: Score 386.4; DB 4; Length 390;
 Best Local Similarity 99.7%: Pred. No. 4.6e-117;
 Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 968 AGGTACAAAGCCCTACTCCAAAGACTGCAGCTTGAAGATAAAGAGAGCACTGCGCTCTT 1027
 DB 1 AAGTACAAAGCCCTACTCCAAAGACTGCAGCTTGAAGATAAAGAGAGCACTGCGCTCTT 60
 QY 1028 TGAATAATTAAGGCGAGACACAAAGAAAGAGAGCTACTTACCCAGCATTTACCTGCGG 1087
 DB 61 TGAATAATTAAGGCGAGACACAAAGAAAGAGAGCTACTTACCCAGCATTTACCTGCGG 120
 QY 1088 GATGTCCTCTCCATCTTATTTTACCTGGTGTGTAATCCGAGCATTTCTTAAAGG 1147
 DB 121 GATGTCCTCTCCATCTTATTTTACCTGGTGTGTAATCCGAGCATTTCTTAAAGG 180
 QY 1148 CATTTTGGCAGCCCTGTGTGACTATACCACTGACAGTGTGAAAGCGCAGGCTACAGG 1207
 DB 181 CATTTTGGCAGCCCTGTGTGACTATACCACTGACAGTGTGAAAGCGCAGGCTACAGG 240
 QY 1208 AGCTGTGAGTAAACAAAGGGGACAGCCGATTTAGCCGTTTGTACAGAGATGCTGTGCT 1267
 DB 241 AGCTGTGAGTAAACAAAGGGGACAGCCGATTTAGCCGTTTGTACAGAGATGCTGTGCT 300
 QY 1268 GCTTGTGAGATCTCTCTGCTTCCCTTCTTGCGACAGCCACTGAGTCTCCTGCTCG 1327
 DB 301 GCTTGTGAGATCTCTCTGCTTCCCTTCTTGCGACAGCCACTGAGTCTCCTGCTCG 360
 QY 1328 AACATCTTCTTAAACTTCAACCCAGAGC 1355
 DB 361 AACATCTTCTTAAACTTCAACCCAGAGC 388

RESULT 3

US-08-365-486A-18
 Sequence 18, Application US/08365486A
 Patent No. 5834306
 GENERAL INFORMATION:
 APPLICANT: Webster, Keith A.
 APPLICANT: Bishopric, Nanette H.
 TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/365,486A
 FILING DATE: 23-DEC-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 8255-0018
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4353 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al,
 INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..4305
 US-08-365-486A-18

Query Match 3.1%: Score 64.6; DB 2; Length 4353;
 Best Local Similarity 48.9%: Pred. No. 2.2e-10;
 Matches 244; Conservative 0; Mismatches 239; Indels 16; Gaps 2;

QY 1588 TTCACCTTACCATGATGACCCCTCAATCCCATATATATGTTGCTCCAGAACCGGCATTA 1647
 DB 3715 TTCCACCTTACCATGATGACCCCGAAGCCCATGATCTGTTGACACAGAACCGGCATTT 3774
 QY 1648 GCCCGCTTATTTGGTCTCAACATAGAACTCCAGAA-CACACCCGATGGAAT 1706
 DB 3775 GCCCGCTTCCGAAAGTTCTGCGACAGCGCAATTTGATTCACACAGAAAGAAATGAAAC 3834
 QY 1707 TTTGAGCAGATGTTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1766
 DB 3835 CCGTGGCCCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3894
 QY 1767 AAAGAGCTCAGACATTTCTTACGATGGATCTTAATCTTAAGAGTTCTTCTTCA 1826
 DB 3895 GAAGAGACCTTGCAGAGCCCAAGAACAGGGGCTTTCAGAGAGCTGTACACGCTTACTCC 3954
 QY 1827 AGAGATGCTCTGTTGGGAG 1886
 DB 3955 C-----GGAG 3999
 QY 1887 CTTATGCGCAGAGAGTGGGAGAGATCTCTCCAGAGAAAGCCATATTATGTTGTT 1946
 DB 4000 GAGCAGCTGGGAGAGTGTGTACCGAGCCCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4059
 QY 1947 GGAGATGCAAAAGATATATGCGCCAGAGATGTATGATGCTTGTGCTTGTGCTTGTGCTTGTG 2006
 DB 4060 TGTGGGAGAGTCCACCATGCTGTGATGTCTTCAAAAGCATTCACAGGATCATGTGACCGAG 4119
 QY 2007 GAGGTGAGATTGAAAACTGAAGACATGAAAGAAAGCCAGGACATTTTAAAGAGAGAGAGAA 2066
 DB 4120 CAGGGGAAGCTCTCGGACAG 4179
 QY 2067 CGTACCTTCAGGATATT 2085
 DB 4180 CGATACCATGAGGATATT 4198

RESULT 4
 US-08-880-342-18

Sequence 18 Application US/0880342
Patent No. 6218179

GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 4353 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al,
INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4305

US-08-880-342-18

Query Match 3.1%; Score 64.6; DB 4: Length 4353;
Best Local Similarity 48.9%; Pred. No. 2.2e-10;
Matches 244; Conservative 0; Mismatches 239; Indels 16; Gaps 2;

OY 1588 TTCACACTTACCAGATGACCCCTCATATCCCCTCATTAATGGTGCGTCGACGAACCGGCATA 16477
||||| || | |||| | |||| | || | || |||| | |||||
Db 3715 TTCACACTGCCCGCGAAGACCCCAAGTCCCTGCATCCTCGTTGGACCAAGGACCGGCATT 3774
||||| || | |||| | |||| | || | || |||| | |||||
OY 1648 GCCCCGTTTATGGGTTCCTACAACATAGAAGATCCCAAGAA-CAACACCCAGATGGAAT 1706
||||| || | |||| | |||| | || | || |||| | |||||
Db 3775 GCCCCTTTCGCAACCTTCTGCGCACAGCGCAATTGTGATTCACAAACAAAGGATGAAC 3834
||||| || | |||| | |||| | || | || |||| | |||||
OY 1707 TTGGAGACATGTCGTTGTTTTTTTGGCTCGCAGCATAGAGTAGGATTAATCTATTCGA 1766
||||| || | |||| | |||| | || | || |||| | |||||
Db 3835 CCCTGCCCATAGTCTGCTGCTTTGGGGTCCGCGCAATCCAAGATGATCATATCTACAGG 3894

[illegible]

RESULT 5
 US-08-365-486A-20
 Sequence 20. Application US/08365486A
 Patent No. 5834306
 GENERAL INFORMATION:
 APPLICANT: Webster, Keith A.
 APPLICANT: Bishopic, Nanette H.
 TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 TITLE OF INVENTION: Therapeutic Constructs
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/365,486A
 FILING DATE: 23-DEC-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 8255-0018
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ. ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4780 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human NOS-3N gene, Nakane, et al
 INDIVIDUAL ISOLATE: PBES Lett 316:175 (1993)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 431..4732

Db 4262 CCCTGCCCATGTCCTGCTTCGGGTGCGCCGCAATCCAGATGATCATCTACAGG 4321
QY 1767 AAGAGCTCAGACATTTCTTAAAGCATGGGATCTTAACATCTAAAGGTTCTCTCA 1826
Db 4322 GAAGAGACCTCGAGCCCAAGAACAGGGGCTCTTAGAGAGTGTACACGGCTTACTCC 4381
QY 1827 AGAGATGCTCTTGGGAGGAGGAGAACCCCGCAAGATGTTACAGACAAATCCAG 1886
Db 4382 C-----GGAGAGCCAGCAAAACCAAGACGACTGACGACATCTGACG 4426
QY 1887 CTTCATGGCCAGAGGTGGCGAAGAACTCTCCAGAGAGAGCCATATTTATGTGTG 1946
Db 4427 GAGCAGCTGGCGAGCTGTGTATCCAGAGCCCTGAGAGAGAGAGGCGCCACATATACGTC 4486
QY 1947 GAGATGCAAGAAATATGSCCAAGATGATGATGATGATGATGATGATGATGATGAT 2006
Db 4487 TGTGGGAGCTGACCATGCTGCTGTGTGTCTCAAGGATCCAGGCAATGATGACCCAG 4546
QY 2007 GAGGTGGATGGAAGAACTAGAACGATGAAACCTTGCCACTTTAAAGAGAAAA 2066
Db 4547 CAGGGGAAGCTCTCGGAGAGAGAGCGCGGCTATTTCATGACCGGATGAGGATGACAC 4606
QY 2067 CGCTACCTTCAGATATTT 2085
Db 4607 CGATACCATGAGGATATTT 4625

RESULT 8
US-08-880-342-20

; Sequence 20, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4780 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human MOS-SN gene, Nakane, et al,
; INDIVIDUAL ISOLATE: FEBS Lett 316:175 (1993)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 431..4732
; US-08-880-342-20

Query Match 3.1%; Score 64.6; DB 4; Length 4780;
Best Local Similarity 48.9%; Pred. No. 2.4e-10;
Matches 244; Conservative 0; Mismatches 239; Indels 16; Gaps 2;

QY 1588 TTCACCTTACAGATGACCCCTCAATCCCATATATGATGATGATGATGATGATGATGAT 1647
Db 4142 TTCACCTTACAGATGACCCCTCAATCCCATATATGATGATGATGATGATGATGATGAT 4201
QY 1648 GCGCGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1706
Db 4202 GCGCGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4261
QY 1707 TTTGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1766
Db 4262 CCCTGCCCATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4321
QY 1767 AAGAGCTCAGACATTTCTTAAAGCATGGGATCTTAACATCTAAAGGTTCTCTCA 1826
Db 4322 GAAGAGACCTCGAGCCCAAGAACAGGGGCTCTCAGAGACTGTACAGGCTTATCC 4381
QY 1827 AGAGATGCTCTGTTGGGAG 1886
Db 4382 C-----GGAGAGCCAGCAAAACCAAGACGACTGACGACATCTGACG 4426
QY 1887 CTTCATGGCCAGAGGTGGCGAAGAACTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1946
Db 4427 GAGCAGCTGGCGAGCTGTGTATCCAGAGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 4486
QY 1947 GAGATGCAAGAAATATGSCCAAGATGATGATGATGATGATGATGATGATGATGATGAT 2006
Db 4487 TGTGGGAGCTGACCATGCTGCTGTGTGTCTCAAGGATCCAGGCAATGATGACCCAG 4546
QY 2007 GAGGTGGATGGAAGAACTAGAACGATGAAACCTTGCCACTTTAAAGAGAAAA 2066
Db 4547 CAGGGGAAGCTCTCGGAGAGAGAGCGCGGCTATTTCATGACCGGATGAGGATGACAC 4606
QY 2067 CGCTACCTTCAGATATTT 2085
Db 4607 CGATACCATGAGGATATTT 4625

RESULT 9

; Sequence 12, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: rat bmos cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 349..4638
US-08-365-486A-12

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Query Match	2.98;	Score 59.8;	DB 2;	length 5057;
Best Local Similarity	48.38;	Pred. No. 9.3e-09;		
Matches 241; Conservative	0;	Mismatches 242;	Indels 16;	Gaps 2

QY	1588	TTTCACATTACAGATGACACCCCTCAATCCCTCTTAATGGTGGGCGAGAAACCGGCTA	1647
Db	4048	TTCCACTGCTCGAAACCCCCAGTGCTTGATCTCGGTGGGCCAGGCACTGGCATC	4107
QY	1648	GCCCGCTTTATTTGGGCTTCTACAAACATGAAACTCCAGAA - CAACACCCGATGGAAT	1706
Db	4108	GCACCCCTTCGMACTCTTGCAACAGGACAAATTTGACATCCAAACAAAGGAATGAT	4167
QY	1707	TTTGAGACAATGTGGTGTGTTTTGGCGCAGGACATAGGATPAGGATATATCTATTCAGA	1766
Db	4168	CCGTGGCCCATGTTCTTGTTTGGGGTGTGCACAAATCCAAAGATAGATCATATCTACAGA	4227
QY	1767	AAAGAGCTCAGACATTTCTTAAACATGGGATCTTAACTCATCTAAAGGTTTCTCTCA	1826
Db	4328	GAGGAGACCCCTGCAGGCTAAGAACAGGGGCTTTGACAGAGAGTGTAACACTGGCTATTC	4287
QY	1827	AGAAATGTCCTCTGTTGGGAGGAGAGAAACCCACAGAAAGTATGTACAAAGACAAATCCAG	1886
Db	4288	CGGGAAACC-----GGACAGGCGCAAGAAATATGTACAGAGAGCTGCTGTG	4332
QY	1887	CTTATGATGGCCAGCAGTGCGGAGAGATCCTCCCTCCAGAGAAACGGCCATATTTATGTGCT	1946
Db	4333	GAACAGCTGGCTGAGTCTGTGTACCGGGCCCTGAAGAGCAAGAGAGGCCACATTTATGTC	4392
QY	1947	GGAAATGCAAAGATATATGCCCAGAGATGTACATGATGCTCTTGCAAAATATATAACAA	2006
Db	4393	TGTGGGGACGTTTACCATATGGCGCGCGATGTCTCTCAAGGCAATCCAGCGCATATATGACCG	4452
QY	2007	GAGCTTGAGATGAAAAAACAATGAAGCAATGAAAACCCCTGGCCACTTTAAAAAGAAAAA	2066
Db	4453	CAGGGAAACATCTCAGAGAGAGAGAGCTGTGTATTTCATCACAGAGCTGAGGATGACAAAC	4512
QY	2067	CGCTACCTTCAGGATATTT	2085
Db	4513	CGGTACCAACGAGGACATCT	4531

RESULT 10
US-08-880-342-12

Sequence 12, Application US/0880342
Patent No. 6218179

GENERAL INFORMATION:

APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.

TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996

APPLICATION NUMBER: PCT/IB95/00996
 FILING DATE: 13-NOV-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/365,486
 FILING DATE: 23-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 8255-0018.30
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5057 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cdna to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: rat bnos cdna
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 349..4638
 OS-08-880-342-12

	Query Match	Best Local Similarity	Score 59.8	DB 4	Length 5057
	Matches 241	Conservative 0	Mismatches 242	Indels 16	Gaps 2
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QY	1767	AAAGAGCTCAGACATTTTCCCTTAAGCATGGGATCTTAACTCATCTTAAAGGTTTCTCTCA	1826		

Db	4228	GAGGAGACCCCTGCAGGGCTAAGACACAGGGGGCTCTTCACAGAGGCTGTACACTGCCATATCC	4287
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Db	4288	CGGGAAAC-----GGACAGGGCCAAAGAAATGTATGACAGAGCGTCTCGAG	4332
Qy	1887	CTTATGCGCCAGCAGGTGGCGAGAAATCCTCTCCAGGAGAACGGCCATTTATGTGTGT	1946
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Qy	1947	GGAGATGCMAAAGAAATATGGCCCAAGAGATGCATGATGCCCTTGTGCAATATATAAGCAAA	2060
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Qy	2007	GAGGTTGGAGTTGAAAAACTTGAAGCAATGAAAAACCTGGCCACTTTAAAGAAAGAAAA	2066
Db	4453	CAGGGCAAACTCTCAGAGGAGAGCGTGTATTTCATCACAGGCTGAGGAGATGACAAAC	4512
Qy	2067	CGTACCGTTCGAGATATTT	2085
Db	4513	CGGTACACGAGGACATCT	4531

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RESULT 11
US-07-642-002-1
: Sequence 1, Application US/07642002
: Patent No. 5268465
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: GENERAL INFORMATION:
: APPLICANT: Bredt, David S.
: APPLICANT: Hwang, Paul M.
: APPLICANT: Reed, Randall
: APPLICANT: Snyder, Solomon H.
: TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
: TITLE OF INVENTION: Oxide Synthase
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Banner, Birch, McKie & Beckett
: STREET: One Thomas Circle, NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/642,002
: FILING DATE: 19910118
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Kagan, Sarah A.
: REGISTRATION NUMBER: 32,141
: REFERENCE/DOCKET NUMBER: 1107_033576
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 296-5500
: TELEFAX: (202) 296-7830
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5108 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: N
: ANTI-SENSE: N
: ORIGINAL SOURCE:
: ORGANISM: Rattus rattus
: TISSUE TYPE: Brain
: FEATURE:
: NAME/KEY: CDS

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; LOCATION: 400..4686
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; OTHER INFORMATION:
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US-07-642-002-1

Query Match	2.9%	Score 59.8;	DB 1;	Length 5108;
Best Local Similarity	48.3%;	Pred. No. 9.4e-09;		
Matches 241;	Conservative	0;	Mismatches 242;	Indels 16; Caps 2

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QY	1648	GCCTCGTTTATGGGTCTTACAAACATAGAAGCTCCAGAA-CAACACCCAGATGGAAAT	1708
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QY	1707	TTTGAGCAATATGTGGTGTTTTGGCTGGCAGGCAATAGGATAGGAGATTAATCTATTCAGA	1766
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QY	2007	GAGCTTGAGATTGAAAAACTAGAAGCAATGAAAAACCTGCGCACATTAAAGAAAGAAAAA	2066
Db	4504	CAGGGAAAGCTCTCAGAGGAGGAGCGTGTGTATTTCATCAGCAGAGGCTGAGGAGATGACAAAC	4566
QY	2067	CGCTACCTTCAGGATATTT	2085
Db	4564	CGGTACCACGAGGACATCT	4582

RESULT 12

US-09-627-216A-13
; Sequence 13, Application US/09627216A

; Patent No. 6368837
; GENERAL INFORMATION:
; INFORMATION:

APPLICANT: Tang, Xiao-Song

APPLICANT: Vannelli, Todd
APPLICANT: Gatenby, Anthony

FILE REFERENCE: BC1009 US NA

; CURRENT APPLICATION NUMBER: US/09/627, 216A
 ; CURRENT FILING DATE: 2000-07-27

;; PRIOR APPLICATION NUMBER: 60/
;; PRIOR FILING DATE: 1999-08-06

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; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97

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; SEQ ID NO 13
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; LENGTH: 1863
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; TYPE: DNA

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ORGANISM: Helianthus tuberosus
US-09-627-216A-13

US-09-627-216A-13

Query Match	2.7%;	Score 56;	DB 4;	Length 1863;
Best Local Similarity	49.0%;	Pred. No. 8.4e-08;		
Matches 253;	Conservative 0;	Mismatches 240;	Indels 23;	Gaps 3;

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: July 29, 2003, 10:56:19 ; Search time 424.273 Seconds
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Title: US-09-371-347a-47
Perfect score: 2093
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2093	100.0	2093	US-09-371-347-47	Sequence 47, Appl
2	2079	99.3	2097	US-09-371-347-1	Sequence 1, Appl
3	2079	99.3	3259	US-09-371-347-24	Sequence 24, Appl
4	2077.4	99.3	2097	US-09-371-347-41	Sequence 41, Appl
5	2077.4	99.3	2097	US-09-371-347-43	Sequence 43, Appl
6	2063	98.6	2094	US-09-371-347-45	Sequence 45, Appl
7	174.4	8.3	2475	US-09-909-567B-38	Sequence 38, Appl
8	83	4.0	1872	US-09-917-800A-1351	Sequence 1351, Ap
9	83	4.0	2401	US-09-917-800A-1357	Sequence 1357, Ap
10	79.6	3.8	101	US-09-783-590-1364	Sequence 1364, Ap
11	65	3.1	298	US-09-294-093B-4842	Sequence 4842, Ap
12	64	3.1	230	US-09-923-876-2845	Sequence 278, App
13	60.4	2.9	2470	US-09-832-849A-278	Sequence 803, App
14	58.4	2.8	2136	US-09-938-842A-803	Sequence 13, Appl
15	56	2.7	1863	US-09-765-873A-13	Sequence 3039, Ap
16	55.6	2.7	2403	US-09-880-107-3039	

17	53	2.5	411	10	US-09-925-299-440	Sequence 440, App
18	53	2.5	411	12	US-09-925-299-440	Sequence 440, App
19	52.8	2.5	13508	8	US-08-781-986A-120	Sequence 120, App
20	51.4	2.5	2088	15	US-10-128-714-7234	Sequence 7234, App
21	50.2	2.4	1448	15	US-09-939-980-113	Sequence 113, App
22	48.4	2.3	1944	10	US-10-272-017A-4	Sequence 4, Appl
23	48.4	2.3	3037	10	US-09-911-781-10	Sequence 10, Appl
24	48.4	2.3	4145	10	US-09-911-781-3	Sequence 3, Appl
25	48.4	2.3	4145	12	US-09-976-800-82	Sequence 82, Appl
26	48.4	2.3	4145	15	US-10-138-838-82	Sequence 82, Appl
27	48.4	2.3	4145	15	US-10-139-031-82	Sequence 82, Appl
28	48.4	2.3	4145	15	US-10-138-905-82	Sequence 82, Appl
29	48.4	2.3	4145	15	US-10-138-916-82	Sequence 82, Appl
30	48.4	2.3	4957	11	US-10-201-213-1	Sequence 1, Appl
31	47.6	2.3	1791	15	US-09-778-319-1	Sequence 1, Appl
32	47.2	2.3	1845	15	US-10-128-714-1234	Sequence 1234, Ap
33	47.2	2.3	1845	15	US-10-128-714-2234	Sequence 2234, Ap
34	47.2	2.3	2145	15	US-10-128-714-6234	Sequence 6234, Ap
35	47.2	2.3	3845	15	US-10-128-714-234	Sequence 234, App
36	47.2	2.3	4145	15	US-10-128-905-81	Sequence 81, Appl
37	46.8	2.2	1944	15	US-10-272-017A-1	Sequence 1, Appl
38	46.8	2.2	4206	10	US-09-911-781-2	Sequence 2, Appl
39	46.8	2.2	4206	12	US-09-976-800-81	Sequence 81, Appl
40	46.8	2.2	4206	15	US-10-138-838-81	Sequence 81, Appl
41	46.8	2.2	4206	15	US-10-139-031-81	Sequence 81, Appl
42	46.8	2.2	4206	15	US-10-138-905-81	Sequence 81, Appl
43	46.8	2.2	4206	15	US-10-138-916-81	Sequence 81, Appl
44	46.6	2.2	1989	11	US-09-974-300-2023	Sequence 2023, Ap
45	44	2.1	640681	11	US-09-790-988-1	Sequence 1, Appl

ALIGNMENTS

US-09-371-347-47	Sequence 47, Application US/09371347
US-09-371-347-1	Publication No. US20030082676A1
GENERAL INFORMATION:	
APPLICANT:	Roy A. Gravel et al.
TITLE OF INVENTION:	HUMAN METHIONINE SYNTHASE REDUCTASE:
TITLE OF INVENTION:	CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
FILE REFERENCE:	50004/003003
CURRENT APPLICATION NUMBER:	US/09/371,347
CURRENT FILING DATE:	1999-08-10
PRIOR APPLICATION NUMBER:	60/071,622
PRIOR FILING DATE:	1998-01-16
PRIOR APPLICATION NUMBER:	09/232,028
PRIOR FILING DATE:	1999-01-15
NUMBER OF SEQ ID NOS:	51
SOFTWARE:	FastSeq for Windows Version 4.0
SEQ ID NO 47	
LENGTH:	2093
TYPE:	DNA
ORGANISM:	Homo sapiens
US-09-371-347-47	
Query Match	100.0%; Score 2093; DB 12; Length 2093;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 2093:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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121	TCGATTAAGTATGACCTAAACCAACAGCTCTCTGTGTTGTGTTGTTACACAG 180

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181 GGCACCGAGACCCGACACAGCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
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361 CGGATTTCTATGACACTGACATGACATGACTGTAGAGTTTGAAGCTTGCTGTTAG 420
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RESULT 2
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Sequence 1, Application US/09371347
Publication No. US20030082676A1
GENERAL INFORMATION:
APPLICANT: Roy A. Gravel et al.
TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
TITLE OF INVENTION: CLONING AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371,347
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/071,622
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/232,028
PRIOR FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2097
TYPE: DNA
ORGANISM: Homo sapiens
US-09-371-347-1

Query Match 99.3%; Score 2079; DB 12; Length 2097;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

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661 ATTGAAGACTTGAAGTCTCACTTACCCGTTGCGTACCCCACTGCACAAAGCCTCTCG 720
721 AATATTCTGCTTTACCCCGCAAAATATTACAGGTACATCTCAGAGAGTCTTGTGGCCAG 780
721 AATATTCTGCTTTACCCCGCAAAATATTACAGGTACATCTCAGAGAGTCTTGTGGCCAG 780
781 GAGGAAGCAGATCTGTGACTCAGAGATCCAGTTTTCAGAGTTCGCAATTTCAAG 840
781 GAGGAAGCAGATCTGTGACTCAGAGATCCAGTTTTCAGAGTTCGCAATTTCAAG 840
841 GCAGTTCACTTACTACGAATGATGCATAAACCACTCTCTGTTAGATTGGACATT 900
841 GCAGTTCACTTACTACGAATGATGCATAAACCACTCTCTGTTAGATTGGACATT 900
901 TCAAAATACAGACTTTTCTATCAGCCTGAGATGCTTTCAGCGTATCTGCCCTAACAT 960

||||| 901 TCAAAATACAGACTTTTCTATCAGCCTGAGATGCTTTCAGCGTATCTGCCCTAACAT 960
961 GATTTCTGAGTCAAGAGCTTACTCCAAAGACCTGAGCTTGAAGATTAAGAGACACTGC 1020
961 GATTTCTGAGTCAAGAGCTTACTCCAAAGACCTGAGCTTGAAGATTAAGAGACACTGC 1020
1021 GTCTTTTGAATAATTAAGGACAGACAAAGAAAGAGAGTACCTTACCCAGCATATTA 1080
1021 GTCTTTTGAATAATTAAGGACAGACAAAGAAAGAGAGTACCTTACCCAGCATATTA 1080
1081 CCTGGGGATTTCTCTCAGTTCAATTTTACCTGGTGTCTTGAATCCGAGCAATTCCT 1140
1081 CCTGGGGATTTCTCTCAGTTCAATTTTACCTGGTGTCTTGAATCCGAGCAATTCCT 1140
1141 AAAAAAGCAATTTTTCGAGCCCTTGTGACTATACCAGTGCAGCTGTGAAGGCGCAGG 1200
1141 AAAAAAGCAATTTTTCGAGCCCTTGTGACTATACCAGTGCAGCTGTGAAGGCGCAGG 1200
1201 CTACAGAGCTGTGAGTAAACAAAGGGGAGCGGATTAATAGCCGCTTGTACAGATGCC 1260
1201 CTACAGAGCTGTGAGTAAACAAAGGGGAGCGGATTAATAGCCGCTTGTACAGATGCC 1260
1261 TGTGCTGCTTGTGATCTCTCTCGCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 1320
1261 TGTGCTGCTTGTGATCTCTCTCGCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 1320
1321 CTGCTGCAACATCTTCTTAACTTCAACCCACACCATATCTGCTGTGCAAGCTCAAGTTA 1380
1321 CTGCTGCAACATCTTCTTAACTTCAACCCACACCATATCTGCTGTGCAAGCTCAAGTTA 1380
1381 TTTCAACCCAGGAACCTCCTTCTTCAACATTTGAGATTTCTGCTCTGACCA 1440
1381 TTTCAACCCAGGAACCTCCTTCTTCAACATTTGAGATTTCTGCTCTGACCA 1440
1441 ACAGAGTTCTGCGGAAGGAGATGTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1441 ACAGAGTTCTGCGGAAGGAGATGTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1501 CTTCAGCCCAACATATCATGATCCCATGAAAGACAGCGGAAAGCCCTGCTCTAAGATA 1560
1501 CTTCAGCCCAACATATCATGATCCCATGAAAGACAGCGGAAAGCCCTGCTCTAAGATA 1560
1561 TCCATCTCTCTGCAACCAAAATCTTCCACTTACAGATGAGCCCTCAATCCCATATC 1620
1561 TCCATCTCTCTGCAACCAAAATCTTCCACTTACAGATGAGCCCTCAATCCCATATC 1620
1621 AATATGTTGGTTCAGGAACCGGATAGCCCGCTTATTTGGTCTTACACAT - - - AG 1676
1621 AATATGTTGGTTCAGGAACCGGATAGCCCGCTTATTTGGTCTTACACAT - - - AG 1676
1677 AATCTCAAGAACCAACACCAAGTGAATTTTGAAGCAATGTGTTTGTGCTGCTC 1736
1677 AATCTCAAGAACCAACACCAAGTGAATTTTGAAGCAATGTGTTTGTGCTGCTC 1736
1681 AATCTCAAGAACCAACACCAAGTGAATTTTGAAGCAATGTGTTTGTGCTGCTC 1740
1681 AATCTCAAGAACCAACACCAAGTGAATTTTGAAGCAATGTGTTTGTGCTGCTC 1740
1737 AGGCAATAGGATAGGATTAATCTATTCAGAAAAAGAGCTAGACATTTCTTAAGCATGG 1796
1737 AGGCAATAGGATAGGATTAATCTATTCAGAAAAAGAGCTAGACATTTCTTAAGCATGG 1796
1741 AGGCAATAGGATAGGATTAATCTATTCAGAAAAAGAGCTAGACATTTCTTAAGCATGG 1800
1741 AGGCAATAGGATAGGATTAATCTATTCAGAAAAAGAGCTAGACATTTCTTAAGCATGG 1800
1797 ATCTTAACATCAATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1856
1797 ATCTTAACATCAATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1856
1801 ATCTTAACATCAATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
1801 ATCTTAACATCAATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
1857 CCAGCAAGTATGTCAAGACAAATCCAGCTTCAATGGCCAGAGGTGGCGAGATTCCTC 1916
1857 CCAGCAAGTATGTCAAGACAAATCCAGCTTCAATGGCCAGAGGTGGCGAGATTCCTC 1916
1861 CCAGCAAGTATGTCAAGACAAATCCAGCTTCAATGGCCAGAGGTGGCGAGATTCCTC 1920
1861 CCAGCAAGTATGTCAAGACAAATCCAGCTTCAATGGCCAGAGGTGGCGAGATTCCTC 1920
1917 CTTCAGGAGAAAGGCCATATTTATGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1976
1917 CTTCAGGAGAAAGGCCATATTTATGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1976
1921 CTTCAGGAGAAAGGCCATATTTATGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1980
1921 CTTCAGGAGAAAGGCCATATTTATGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1980
1977 CATGATGCCCTTGTCAAAATTAATTAAGCAAGAGTTTGAAGAACTAGAACCAATG 2036
1977 CATGATGCCCTTGTCAAAATTAATTAAGCAAGAGTTTGAAGAACTAGAACCAATG 2036

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Db      1981 CATGATGCCCTTGTGCAAAATATATAGCAAGAGTTGAGTTGAAAACTAGAACGAATG 2040
QY      2037 AAAACCCCTGGCCACTTTAAAGAGAAAGAAACCGCTACTCTAGATATTTGGTCATA 2093
Db      2041 AAAACCTGGCCACTTTAAAGAGAAAGAAACCGCTACTCTAGATATTTGGTCATA 2097

RESULT 3
US-09-371-347-24
; Sequence 24, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT FILING DATE: US/09/371,347
; PRIOR FILING DATE: 1999-08-10
; PRIOR FILING DATE: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 3259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-24

Query Match      99.3%; Score 2079; DB 12; Length 3259;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY      1  ATGAGAGGTTCTGTACTATATGCTACAGCAGGAGGCAAGGCCATCGCAGA 60
Db      80  ATGAGAGGTTCTGTACTATATGCTACAGCAGGAGGCAAGGCCATCGCAGA 139
QY      61  GAAATGTGTAGCAAGCTGTGTACATGATTTTTCAGATCTTCATCTGATTAAGTGA 120
Db      140  GAAATGTGTAGCAAGCTGTGTACATGATTTTTCAGATCTTCATCTGATTAAGTGA 199
QY      121  TCCGATTAAGTATGACTTAAGAAACCGAAAGAGTCCCTCTTGTGTGTCTTACACG 180
Db      200  TCCGATTAAGTATGACTTAAGAAACCGAAAGAGTCCCTCTTGTGTGTCTTACACG 259
QY      181  GGCACCGGAGACCCACCCGACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
Db      260  GGCACCGGAGACCCACCCGACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 319
QY      241  CTGCGGTTGATTTCTTCTCACTGCGGTATGGGTACTGGTCTGCGTATTCAGAA 300
Db      320  CTGCGGTTGATTTCTTCTCACTGCGGTATGGGTACTGGTCTGCGTATTCAGAA 379
QY      301  TACACCTACTTTTGAATGGGGGGAAGATTAATTGATTAACGACTTCAAGCTTGAGCC 360
Db      380  TACACCTACTTTTGAATGGGGGGAAGATTAATTGATTAACGACTTCAAGCTTGAGCC 439
QY      361  CGGCATTTCTATGACATGAGATGATGATGATGATTTTGAATTTGATTTGGTGG 420
Db      440  CGGCATTTCTATGACATGAGATGATGATGATGATTTTGAATTTGATTTGGTGG 499
QY      421  CCGTGGATTTGCTGACTGTGGCCAGCCCTCAGAAAGCATTTTAAAGTCAAGAGAGACA 480
Db      500  CCGTGGATTTGCTGACTGTGGCCAGCCCTCAGAAAGCATTTTAAAGTCAAGAGAGACA 559
QY      481  GAGGAGATTAAGTGGGCACTCCCGGTGCATCACTGCATCTTTAGAGCAGACCTTGTG 540
Db      560  GAGGAGATTAAGTGGGCACTCCCGGTGCATCACTGCATCTTTAGAGCAGACCTTGTG 619
QY      541  AAGTGAAGCTCTACATTAATCTCAAGTCGAGCTTCTGAGATTCGATTCAGGA 600

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Db      620  AAGTCAGAGCTCTACATGATTAATCTCAAGTCGAGCTTCTGAGATTCGATTCAGGA 679
QY      601  AGAAGAGATTCGAGGTTTGAAGCAAAATGCAAGCAAGCAACCAATCCATGTGTGA 660
Db      680  AGAAGAGATTCGAGGTTTGAAGCAAAATGCAAGCAAGCAACCAATCCATGTGTGA 739
QY      661  ATTGAAGATTCGAGGTTTGAAGCAAAATGCAAGCAAGCAACCAATCCATGTGTGA 720
Db      740  ATTGAAGATTCGAGGTTTGAAGCAAAATGCAAGCAAGCAACCAATCCATGTGTGA 799
QY      721  AATATTCCTGCTTTTACCCCAAGATTTTACAGATGATCTGAGAGATCTTGTGGCAG 780
Db      800  AATATTCCTGCTTTTACCCCAAGATTTTACAGATGATCTGAGAGATCTTGTGGCAG 859
QY      781  GAGAAAGCAAGTATCTGTGACTCAGAGATTCAGGTTTCAAGTGCATTTTCAAG 840
Db      860  GAGAAAGCAAGTATCTGTGACTCAGAGATTCAGGTTTCAAGTGCATTTTCAAG 919
QY      841  GCAGTTCAACTTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db      920  GCAGTTCAACTTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 979
QY      901  TCAATATGAGCTTTTCTATGAGCTGAGATGCTTCCAGGATGATGATGATGATGAT 960
Db      980  TCAATATGAGCTTTTCTATGAGCTGAGATGCTTCCAGGATGATGATGATGATGAT 1039
QY      961  GATTCGAGTCAAAAGCTTACCAAGACGCTGAGATGATGATGATGATGATGATGAT 1020
Db      1040  GATTCGAGTCAAAAGCTTACCAAGACGCTGAGATGATGATGATGATGATGATGAT 1099
QY      1021  GTCTTTTGAATTAAGGACAGACACAAAGAAAGAGAGTACTTACCCAGCATATA 1080
Db      1100  GTCTTTTGAATTAAGGACAGACACAAAGAAAGAGAGTACTTACCCAGCATATA 1159
QY      1081  CCTGGGAGATGTTCTCTCAGTTCAATTTTACCTGGTGTCTTGAATCCGAGCAAT 1140
Db      1160  CCTGGGAGATGTTCTCTCAGTTCAATTTTACCTGGTGTCTTGAATCCGAGCAAT 1219
QY      1141  AAAAAGCAATTTTTCGAGACCCCTTGTGAGCTTACAGAGAGAGAGAGAGAGAG 1200
Db      1220  AAAAAGCAATTTTTCGAGACCCCTTGTGAGCTTACAGAGAGAGAGAGAGAGAG 1279
QY      1201  CTACAGAGCTGTGAGTAACAGAGGAGCGGATTAAGCCGTTTGTACAGATGCC 1260
Db      1280  CTACAGAGCTGTGAGTAACAGAGGAGCGGATTAAGCCGTTTGTACAGATGCC 1339
QY      1261  TGTGCTGCTGTTGTGATCTCTCCGCTTTCCTTCTGTCAGACCAACCTCAGTCTC 1320
Db      1340  TGTGCTGCTGTTGTGATCTCTCCGCTTTCCTTCTGTCAGACCAACCTCAGTCTC 1399
QY      1321  CTGCTCGAATCTTCTAATCTCAACCCAGACCATATGCTGTGCAAGCTCAAGTTA 1380
Db      1400  CTGCTCGAATCTTCTAATCTCAACCCAGACCATATGCTGTGCAAGCTCAAGTTA 1459
QY      1381  TTTTCAACCAAGAAAGCTCATTTTGTCTTCAACATTTGGAATTTCTGTCTACGCCACA 1440
Db      1460  TTTTCAACCAAGAAAGCTCATTTTGTCTTCAACATTTGGAATTTCTGTCTACGCCACA 1519
QY      1441  ACAGAGGTTCTGCGGAAGGAGATGATGAGGCTGGGCTGCTGCTGCTGCTGCTGCT 1500
Db      1520  ACAGAGGTTCTGCGGAAGGAGATGATGAGGCTGGGCTGCTGCTGCTGCTGCTGCT 1579
QY      1501  CTTTCAAGCAATCATGATCATCCCATGAAGACAGCGGAAAGCCCTGGCTCTTAAGTA 1560
Db      1580  CTTTCAAGCAATCATGATCATCCCATGAAGACAGCGGAAAGCCCTGGCTCTTAAGTA 1639
QY      1561  TCCATCTCTCTCTGAGAACAAATTTCTTCACTTACAGATGATGATGATGATGATGAT 1620
Db      1640  TCCATCTCTCTCTGAGAACAAATTTCTTCACTTACAGATGATGATGATGATGATGAT 1699
QY      1621  AATATGAGGAGTCCAGGAACCGGCAATAGCCCGTTATTTGGGTTCTCAACAT---AG 1676
Db      1700  AATATGAGGAGTCCAGGAACCGGCAATAGCCCGTTATTTGGGTTCTCAACATAGAGAG 1759

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1677 AAACCTCAAGAACACACACCATGATGAAATTTTGGAGCAATGTGGTGTGTTTGGCTGC 1736
1760 AAACCTCAAGAACACACACCATGATGAAATTTTGGAGCAATGTGGTGTGTTTGGCTGC 1819
1737 AGGATTAAGAGATAGGATTTATCTATTCAGAAAAAGAGCTCAGACATTTCTTAAGCATGG 1796
1820 AGGCATTAAGAGATAGGATTTATCTATTCAGAAAAAGAGCTCAGACATTTCTTAAGCATGG 1879
1797 ATCTTAACATCAATAAAGTTTCCCTTCACAGATGCTCCCTGTTGGGAGAGAGAGCC 1856
1880 ATCTTAACATCAATAAAGTTTCCCTTCACAGATGCTCCCTGTTGGGAGAGAGAGCC 1939
1857 CCAGCAAGATATGTACAGACAAATCCAGCTTCATGAGCAGAGAGAGAGAGATCCCTC 1916
1940 CCAGCAAGATATGTACAGACAAATCCAGCTTCATGAGCAGAGAGAGAGATCCCTC 1999
1917 CTCACAG 1976
2000 CTCACAG 2059
1977 CATGATGCCCTTGTCAAAATTAATAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2036
2060 CATGATGCCCTTGTCAAAATTAATAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2119
2037 AAACCCCTGGCCACTTTTAAAGAAAAAGCAACCTACCTTCAGATATTTGGTCATTA 2093
2120 AAACCCCTGGCCACTTTTAAAGAAAAAGCAACCTACCTTCAGATATTTGGTCATTA 2176

RESULT 4
US-09-371-347-41
Sequence 41, Application US/09371347
Publication No. US20030082676A1
GENERAL INFORMATION:
APPLICANT: Roy A. Gravel et al.
TITLE OF INVENTION: HUMAN MENTIONINE SYNTHASE REDUCTASE:
TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
FILE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371,347
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/071,622
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/232,028
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41
LENGTH: 2097
TYPE: DNA
ORGANISM: Homo sapiens
US-09-371-347-41

Query Match 99.3%; Score 2077.4; DB 12; Length 2097;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2092; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 ATGAGAGAGTTCTGTACTATATGCTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 1 ATGAGAGAGTTCTGTACTATATGCTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 61 GAATGTGTGAGCAAGCTGTGTACATGATTTTTCAGAGATCTTCACTGTATTTAGTGA 120
DB 61 GAATGTGTGAGCAAGCTGTGTACATGATTTTTCAGAGATCTTCACTGTATTTAGTGA 120
QY 121 TCCGATTAAGTATGACTTAATAAACCGAAACAGCTCCTGTTGTGTGTTCTACACAG 180
DB 121 TCCGATTAAGTATGACTTAATAAACCGAAACAGCTCCTGTTGTGTGTTCTACACAG 180
QY 181 GGCACCGGAGACCCGACACAGCCGCGCAAGTTGTTAAGAAATACAGAAACCAACA 240
DB 181 GGCACCGGAGACCCGACACAGCCGCGCAAGTTGTTAAGAAATACAGAAACCAACA 240

QY 241 CTGCCGGTTGATTTCTTTTCTCACCCTGCGGTATGGGTTACTGGGTCTCGGTATTCAGAA 300
DB 241 CTGCCGGTTGATTTCTTTTCTCACCCTGCGGTATGGGTTACTGGGTCTCGGTATTCAGAA 300
QY 301 TACACCTACTTTTGGCAATGGGGGAAAGATTAATGAATTAACGACTTCAGAGCTTGAGCC 360
DB 301 TACACCTACTTTTGGCAATGGGGGAAAGATTAATGAATTAACGACTTCAGAGCTTGAGCC 360
QY 361 CGGATTTTATGACACTGACATGACATGACTGTGTAGTTTGAAGTTTGTGTTGAG 420
DB 361 CGGATTTTATGACACTGACATGACATGACTGTGTAGTTTGAAGTTTGTGTTGAG 420
QY 421 CCGTGATTTGCTGAGACTCTGCGCAGAGCCCTCAGAAAGCATTTTATAGTCAAGAGAGACA 480
DB 421 CCGTGATTTGCTGAGACTCTGCGCAGAGCCCTCAGAAAGCATTTTATAGTCAAGAGAGACA 480
QY 481 GAGAGATTAAGTGGGCACTCCGGTGGCATCCTGCATCTTGTAGAGACAGACCTTGTG 540
DB 481 GAGAGATTAAGTGGGCACTCCGGTGGCATCCTGCATCTTGTAGAGACAGACCTTGTG 540
QY 541 AAGTCAAGACTCTGACATTAATCTCAAGTCTGAGCTTCAAGATTCGATATTCAGAGA 600
DB 541 AAGTCAAGACTCTGACATTAATCTCAAGTCTGAGCTTCAAGATTCGATATTCAGAGA 600
QY 601 AGAAAGATTTGAGGTTTGAAGCAAAATGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 660
DB 601 AGAAAGATTTGAGGTTTGAAGCAAAATGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 660
QY 661 ATTGAAGACTTTGAGTCTCCTACCTACCCCTTGGTGAACCCCACTCTCAGAACCTCTCTG 720
DB 661 ATTGAAGACTTTGAGTCTCCTACCTACCCCTTGGTGAACCCCACTCTCAGAACCTCTCTG 720
QY 721 AATATTCTGTTTACCCCAAGATTTTACAGATTCATCTGACAGAGCTCTTGGCCAG 780
DB 721 AATATTCTGTTTACCCCAAGATTTTACAGATTCATCTGACAGAGCTCTTGGCCAG 780
QY 781 GAGGAAAGCAAGTATCTGTGACTTACAGAGATTCAGAGTTCAGAGTTCAGAGTTCAGAG 840
DB 781 GAGGAAAGCAAGTATCTGTGACTTACAGAGATTCAGAGTTCAGAGTTCAGAGTTCAGAG 840
QY 841 GCAGTTCAACTACTACAGATGATGCAATTAATAAACCACTCTGTTAGAAATTCAGACT 900
DB 841 GCAGTTCAACTACTACAGATGATGCAATTAATAAACCACTCTGTTAGAAATTCAGACT 900
QY 901 TCAAAATACAGACTTTTCTATCAGCCTGAGATGCTTACAGGCTGATCTGCTTACACT 960
DB 901 TCAAAATACAGACTTTTCTATCAGCCTGAGATGCTTACAGGCTGATCTGCTTACACT 960
QY 961 GATTCGAGGTCAAAAGCTTACTCCAAAGACTGACCTTGAAGATTAAGAGAGAGAGAG 1020
DB 961 GATTCGAGGTCAAAAGCTTACTCCAAAGACTGACCTTGAAGATTAAGAGAGAGAGAG 1020
QY 1021 GTCTCTTTGAAATAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 GTCTCTTTGAAATAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 CCTGCGGATGTTTCTCAGTTTCTCAGTTTCTCAGTTTCTCAGTTTCTCAGTTTCTCAG 1140
DB 1081 CCTGCGGATGTTTCTCAGTTTCTCAGTTTCTCAGTTTCTCAGTTTCTCAGTTTCTCAG 1140
QY 1141 AAAAAGCAATTTTGGAG 1200
DB 1141 AAAAAGCAATTTTGGAG 1200
QY 1201 CTACAGAGACTGTGAGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1201 CTACAGAGACTGTGAGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 TGTGCTGCTGTTGATCT 1320
DB 1261 TGTGCTGCTGTTGATCT 1320

[illegible]

|||||
Db 961 GATTCTGAGGTACAAAGCTTACTCCAAAGACTGCAGCTTGAAGATAAAAGAGAGCATGTC 1020
Oy 1021 GTCCCTTTGAAATTAAGGCACACAAAGAAAGAGAGCTACTTACCACGATATA 1080
Db 1021 GTCCCTTTGAAATTAAGGCACACAAAGAAAGAGAGCTACTTACCACGATATA 1080
Oy 1081 CCTGGGGATGTTCTCTCAGTTCAATTTTACCTGGTGCTTGAATCCGAGCAATTCCT 1140
Db 1081 CCTGGGGATGTTCTCTCAGTTCAATTTTACCTGGTGCTTGAATCCGAGCAATTCCT 1140
Oy 1141 AAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTACAGTCTGAAAAAGCGCAG 1200
Db 1141 AAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTACAGTCTGAAAAAGCGCAG 1200
Oy 1201 CTACAGAGCTGTGACATTAACAAAGGGCAGCCGATATAGCCGCTTGTACAGATGCC 1260
Db 1201 CTACAGAGCTGTGACATTAACAAAGGGCAGCCGATATAGCCGCTTGTACAGATGCC 1260
Oy 1261 TGTGCTGCTGTTGTGATCTCCTCGCTTCCCTTTCCTTGGCAGCAGCAGTCTGTC 1320
Db 1261 TGTGCTGCTGTTGTGATCTCCTCGCTTCCCTTTCCTTGGCAGCAGCAGTCTGTC 1320
Oy 1321 CTGCTCGAACAATCTTCTAACTCAACCCAGACCATATTCGTGACAGTCAAGTTTA 1380
Db 1321 CTGCTCGAACAATCTTCTAACTCAACCCAGACCATATTCGTGACAGTCAAGTTTA 1380
Oy 1381 TTTCAACCCAGAAAGCTCATTTTGTCTTCAACATTTTGGAAATTTCTGCTACTGCCACA 1440
Db 1381 TTTCAACCCAGAAAGCTCATTTTGTCTTCAACATTTTGGAAATTTCTGCTACTGCCACA 1440
Oy 1441 ACAGAGTCTCTCGAAGAGGATATGTACAGGCTGGCTGGCTTGTGGTCTCTCAGTT 1500
Db 1441 ACAGAGTCTCTCGAAGAGGATATGTACAGGCTGGCTGGCTTGTGGTCTCTCAGTT 1500
Oy 1501 CTTGAGCCAAACATACATGATCCCATGAAGACAGCGGAAAGCCCTGGCTCTTAAGATA 1560
Db 1501 CTTGAGCCAAACATACATGATCCCATGAAGACAGCGGAAAGCCCTGGCTCTTAAGATA 1560
Oy 1561 TCCATCTCTCTCGAAGCAAAATTTCTTCCATTAACGATGAGCCCTCATTCGCCATC 1620
Db 1561 TCCATCTCTCTCGAAGCAAAATTTCTTCCATTAACGATGAGCCCTCATTCGCCATC 1620
Oy 1621 ATATAGTGTGGTCTCGAAGACCGGCATAGCCGTTTATTTGGTCTCTTACAGAT---AG 1676
Db 1621 ATATAGTGTGGTCTCGAAGACCGGCATAGCCGTTTATTTGGTCTCTTACAGATAGAG 1680
Oy 1677 AAATCTCAAGAACACACCCAGATGGAATTTTGGAGCAATGTGTTTTTGGCTGC 1736
Db 1681 AAATCTCAAGAACACACCCAGATGGAATTTTGGAGCAATGTGTTTTTGGCTGC 1740
Oy 1737 AGGCAATTAAGGATAGGATATATATTTCAGAAAAAGCTAGACATTTCTTAAAGATGG 1796
Db 1741 AGGCAATTAAGGATAGGATATATATTTCAGAAAAAGCTAGACATTTCTTAAAGATGG 1800
Oy 1797 ATCTTAACATCATTAAGGTTTCTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1856
Db 1801 ATCTTAACATCATTAAGGTTTCTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
Oy 1857 CCAGAAAGTATGTACAAAGACATCCAGCTTCATGGCCAGCAGGTCGAGAAATCTTC 1916
Db 1861 CCAGAAAGTATGTACAAAGACATCCAGCTTCATGGCCAGCAGGTCGAGAAATCTTC 1920
Oy 1917 CTCACAGAGAGAGCCCATTTTATGTGTGTGAGATGCAAAAGATATGGCCAAAGATGA 1976
Db 1921 CTCACAGAGAGAGCCCATTTTATGTGTGTGAGATGCAAAAGATATGGCCAAAGATGA 1980
Oy 1977 CATGATGCCCTTGTGCAAAATTAAGCAAAAGAGGTTGAGTTGAAAAACTTAAAGCAATG 2036
Db 1981 CATGATGCCCTTGTGCAAAATTAAGCAAAAGAGGTTGAGTTGAAAAACTTAAAGCAATG 2040
Oy 2037 AAAACCTTGCCCATTTTAAAGAAAAACGCTTACGATATTTTGTCTATTA 2093
|||||

Db 2041 AAAACCTTGCCCATTTTAAAGAAAAACGCTTACTCTTACAGATATTTGTCTATTA 2097
RESULT 6
US-09-371-347-45
; Sequence 45, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE.
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR FILING DATE: 09/232,028
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-45
Query Match 98.6%; Score 2063; DB 12; Length 2094;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2090; Conservative 0; Mismatches 0; Indels 7; Gaps 2;
Oy 1 ATGAGAGAGTTCTGTACTATATGCTACACAGCAGGAGGAGCAAAAGCCATCGCAGAA 60
Db 1 ATGAGAGAGTTCTGTACTATATGCTACACAGCAGGAGGAGCAAAAGCCATCGCAGAA 60
Oy 61 GAAATGTGTGACAGCTGTGTGATGATTTTGTGAGATCTTCACTGATTAAGTGA 120
Db 61 GAAATGTGTGACAGCTGTGTGATGATTTTGTGAGATCTTCACTGATTAAGTGA 120
Oy 121 TCCGATTAAGTATGACTTAAACAAACCAACAGCTCCTCTGTGTGTGTCTTACACAG 180
Db 121 TCCGATTAAGTATGACTTAAACAAACCAACAGCTCCTCTGTGTGTGTGTCTTACACAG 180
Oy 181 GGCACGCGAGACCCACCCGACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
Db 181 GGCACGCGAGACCCACCCGACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
Oy 241 CTGCGGTTGATTTCTTCTCAGCTGCGGTATGGGTACTGGTCTCGGATTTTCAGAA 300
Db 241 CTGCGGTTGATTTCTTCTCAGCTGCGGTATGGGTACTGGTCTCGGATTTTCAGAA 300
Oy 301 TACACCTACTTTTGCATGAGGGGGAAGATTAATTGAATAAACGACTTCAGAGCTTGAGCC 360
Db 301 TACACCTACTTTTGCATGAGGGGGAAGATTAATTGAATAAACGACTTCAGAGCTTGAGCC 360
Oy 361 CGGCAATTTATGACACTGACATGACATGACATGATGATGATTTGAACCTTGGTGGAG 420
Db 361 CGGCAATTTATGACACTGACATGACATGACATGATGATGATTTGAACCTTGGTGGAG 420
Oy 421 CCGTGATTTGCTGAGCTTGGCCAGCCCTCAGAAAGCATTTTAGTCAAGAGAGACAA 480
Db 421 CCGTGATTTGCTGAGCTTGGCCAGCCCTCAGAAAGCATTTTAGTCAAGAGAGACAA 480
Oy 481 GAGGAGATTAAGTGGCGCACTCCCGGTGGCATCCTGATCCTTGTAGAGACAGACTTGTG 540
Db 481 GAGGAGATTAAGTGGCGCACTCCCGGTGGCATCCTGATCCTTGTAGAGACAGACTTGTG 540
Oy 541 AAGTCAGACCTCTACACTTGAATCTCAAGTCAGAGCTTCTAGATTCGATATTCAGGA 600
Db 541 AAGTCAGACCTCTACACTTGAATCTCAAGTCAGAGCTTCTAGATTCGATATTCAGGA 600
Oy 601 AGAAAGATTCGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAATGTGTA 660
|||||

Db 601 AGAAGGATTCGAGTTTGAAGCAAAATGCAGTACAGCAACCAATCAATGTTGTA 660
 QY 661 ATTGAAGACTTTAGTCTCATTACCGCTTGGTACCCCACTCTCACAAGCCCTCTG 720
 Db 661 ATTGAAGACTTTAGTCTCATTACCGCTTGGTACCCCACTCTCACAAGCCCTCTG 720
 QY 721 AATATTCCTGTTTACCCCAAGAAATATTTACAGTACATCTGAGAGAGTCTCTGGCAG 780
 Db 721 AATATTCCTGTTTACCCCAAGAAATATTTACAGTACATCTGAGAGAGTCTCTGGCAG 780
 QY 781 GAGAAAGCCAACTATCTGTGACTGAGATCCAGTTTCAAGTCCCAATTTTCAAG 840
 Db 781 GAGAAAGCCAACTATCTGTGACTGAGATCCAGTTTCAAGTCCCAATTTTCAAG 840
 QY 841 GCAGTCACTTACTACGAATGATGCCATTAACCACTCTGCTGTAGATTGACATT 900
 Db 841 GCAGTCACTTACTACGAATGATGCCATTAACCACTCTGCTGTAGATTGACATT 900
 QY 901 TCAAAATACAGACTTTCTATGAGCGTGGAGATGCTTCAAGCTGATCTGCCCTAACAT 960
 Db 901 TCAAAATACAGACTTTCTATGAGCGTGGAGATGCTTCAAGCTGATCTGCCCTAACAT 960
 QY 961 GATTCTGAGGTACAAAGCCTACTCACAAGCTGCAAGTGAAGATTAAGAGAGCACTGC 1020
 Db 961 GATTCTGAGGTACAAAGCCTACTCACAAGCTGCAAGTGAAGATTAAGAGAGCACTGC 1020
 QY 1021 GTCCCTTTGAAAAATAAGGACAGACAAAGAAAGAGACTACCTTACCCAGCATATA 1080
 Db 1021 GTCCCTTTGAAAAATAAGGACAGACAAAGAAAGAGAGACTACCTTACCCAGCATATA 1080
 QY 1081 CCTGCGGAGATGTTCTCTCAGTTCATTTTACCTGCTGTGAATTCGAGCAATTCCT 1140
 Db 1081 CCTGCGGAGATGTTCTCTCAGTTCATTTTACCTGCTGTGAATTCGAGCAATTCCT 1140
 QY 1141 AAAAGGCAATTTTGGGAGCCCTTGTGACTATACAGTACAGTGTGAAAAAGCCAG 1200
 Db 1141 AAAAGGCAATTTTGGGAGCCCTTGTGACTATACAGTACAGTGTGAAAAAGCCAG 1200
 QY 1201 CTACAGGAGCTGTGCAAGTAAACAAAGGGGAGCCGATTAAGCCGCTTTAGAGATGCC 1260
 Db 1201 CTACAGGAGCTGTGCAAGTAAACAAAGGGGAGCCGATTAAGCCGCTTTAGAGATGCC 1260
 QY 1261 TGTGCTGCTGTTGGATCTCTCCCTGCTTCCCTTCCGAGGACACACATGCTC 1320
 Db 1261 TGTGCTGCTGTTGGATCTCTCCCTGCTTCCCTTCCGAGGACACACATGCTC 1320
 QY 1321 CTGCTCGAATCTTCTTAACCTCAACCCAGACATATTCGTGCAAGTCAAGTTTA 1380
 Db 1321 CTGCTCGAATCTTCTTAACCTCAACCCAGACATATTCGTGCAAGTCAAGTTTA 1380
 QY 1381 TTTCAACCCAGGAAAGCTCATTTTGTCTTCAACATTTGGAATTTCTGTACTGCGACA 1440
 Db 1381 TTTCAACCCAGGAAAGCTCATTTTGTCTTCAACATTTGGAATTTCTGTACTGCGACA 1440
 QY 1441 ACAGAGGTTCTGCGAAGGAGATGTACAGGCTGGCTGCTGTTGTTGTTCTTCAGTT 1500
 Db 1441 ACAGAGGTTCTGCGAAGGAGATGTACAGGCTGGCTGCTGTTGTTGTTCTTCAGTT 1500
 QY 1501 CTTTACGCCAAACATCATGATCCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1560
 Db 1501 CTTTACGCCAAACATCATGATCCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1560
 QY 1561 TCCATCTCTCTCTGCAACAATTTCTTCCATTACAGATGACCCCTCAATGCCCATC 1620
 Db 1561 TCCATCTCTCTCTGCAACAATTTCTTCCATTACAGATGACCCCTCAATGCCCATC 1620
 QY 1621 ATAATGTTGGTCCAGGAACGGCATAGCCCGTTATTTGGTCTCTACACAT ---AG 1676
 Db 1621 ATAATGTTGGTCCAGGAACGGCATAGCCCGTTATTTGGTCTCTACACAT ---AG 1676
 QY 1677 AAATGCTGAGTCCAGGAACGGCATAGCCCGTTATTTGGTCTCTACACAT ---AG 1736
 Db 1677 AAATGCTGAGTCCAGGAACGGCATAGCCCGTTATTTGGTCTCTACACAT ---AG 1736
 QY 1737 AAATGCTGAGTCCAGGAACGGCATAGCCCGTTATTTGGTCTCTACACAT ---AG 1796
 Db 1737 AAATGCTGAGTCCAGGAACGGCATAGCCCGTTATTTGGTCTCTACACAT ---AG 1796

QY 1737 AGGCATTAAGAGTAGGATTAATCTATTCAGAAAAGAGCTGAGACATTTCTTAAGCATGGG 1796
 Db 1738 AGGCATTAAGAGTAGGATTAATCTATTCAGAAAAGAGCTGAGACATTTCTTAAGCATGGG 1797
 QY 1797 ATCTTAATCTATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1856
 Db 1798 ATCTTAATCTATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1857
 QY 1857 CCAGCAAGTATGTACAGCAACATCCAGCTTCATGAGGAGAGAGTGGCGAGATCTTC 1916
 Db 1858 CCAGCAAGTATGTACAGCAACATCCAGCTTCATGAGGAGAGAGTGGCGAGATCTTC 1917
 QY 1917 CTCACAGAGAGAGCCCATATTTATGTGTGAGATGCAAAAGATATGSCCAAGATGTA 1976
 Db 1918 CTCACAGAGAGAGCCCATATTTATGTGTGAGATGCAAAAGATATGSCCAAGATGTA 1977
 QY 1977 CATGATGCCCTTGTGCAATTAATAGCAAAAGAGTTGAGTTGAAAAACTAGAACGATG 2036
 Db 1978 CATGATGCCCTTGTGCAATTAATAGCAAAAGAGTTGAGTTGAAAAACTAGAACGATG 2037
 QY 2037 AAAACCTGGCCACTTAAGAAAGAAAGAAAGCTACCTTCAGGATATTTGGTCATTA 2093
 Db 2038 AAAACCTGGCCACTTAAGAAAGAAAGAAAGCTACCTTCAGGATATTTGGTCATTA 2094

RESULT 7

US-09-567B-38
 ; Sequence 38, Application US/09909567B
 ; Publication No. US20030022257A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Macina, Roberto A.
 ; APPLICANT: Nair, Manoj
 ; APPLICANT: Chen, Selju
 ; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
 ; FILE REFERENCE: DEX-0214
 ; CURRENT APPLICATION NUMBER: US/09/909,567B
 ; PRIOR FILING DATE: 2001-07-20
 ; PRIOR FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 38
 ; LENGTH: 2475
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1001)..(1001)
 ; OTHER INFORMATION: a, c, g or t
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1011)..(1011)
 ; OTHER INFORMATION: a, c, g or t
 ; US-09-909-567B-38

Query Match 8.3%; Score 174.4; DB 12; Length 2475;

Best Local Similarity 96.7%; Pred. No. 9.8e-45;

Matches 178: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 510 ATCAGCTGCATCTTGGAGAGACAGACCTTGTGAAGTCAAGAGTGTACATTAATGATCA 569
 Db 1 ATCAGCTGCATCTTGGAGAGACAGACCTTGTGAAGTCAAGAGTGTACATTAATGATCA 60
 QY 570 AGTCAGGCTTCTGAGATTCGATGATTCAGGAAGAAAGATTCGAGTTTGAAGCAAAA 629
 Db 61 AGTCAGGCTTCTGAGATTCGATGATTCAGGAAGAAAGATTCGAGTTTGAAGCAAAA 120
 QY 630 TGCAGTGAACAGCAACCAATCAATGTTGTAATGAAGACTTGAAGTCTCAGCTTAACCG 689
 Db 121 TGCAGTGAACAGCAACCAATCAATGTTGTAATGAAGACTTGAAGTCTCAGCTTAACCG 180
 QY 690 TTGC 693

Db 181 TTCG 184

RESULT 8

US-09-917-800A-1351
; Sequence 1351, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1351
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 E01524
US-09-917-800A-1351

Query Match 4.0%; Score 83; DB 11; Length 1872;
Best Local Similarity 55.2%; Pred. No. 2,7e-15;
Matches 216; Conservative 0; Mismatches 155; Indels 20; Gaps 2;

QY 1588 TTCACCTTACAGATGATGACCCCTCATTCCTCATATATGTTGGTCCAGAACCGGCATA 1647
DB 1387 TTCCTCTTCCCTTTCAGTCCACACACCTGTCATATGTTGGCCCGGCATGGGATT 1446
QY 1648 GCGCCGTTTATTTGGTCTCTACATCAATGAATCAAGAACACACCCAGATGGAATT 1707
DB 1447 GCGCTTTCATGCGCTTATCATCAGAGAGAGCTTGCTT--CGAAGCAAGCAAGAGAG 1504
QY 1708 TTGAGCAATGTGTTGTTTGGCTGACAGCATTAAGATAGGATTATCTATTCAGAA 1767
DB 1505 TGGGAGAGACGCTGCTATACATATGCTGCGCGCTCGATGAGACTATCTGACCGTG 1564
QY 1768 AAGACTCAGACATTTCTTAAGCATGGATTTAATCATTAAGTTTCTCTCTCAA 1827
DB 1565 AAGACTGAGCCGCTTCCACAGAGAGCGTCCCTCAGCAGCTTATGTTGGCTTTTCCC 1624
QY 1828 GAGATGCTCTGTTGGGAGAGAGAGCCCGCAGCAAGATATGATACAGACATCCAGC 1887
DB 1625 G-----GGAGCAGGCCCAAGGTCTATGTCCAGCACCTTCTGAAAGA 1666
QY 1888 TTCATGCGCAGAGTGCGGAGAAATCTCTTCACAGAGAGCGCATATTTATGTGTGTG 1947
DB 1888 TTCATGCGCAGAGTGCGGAGAAATCTCTTCACAGAGAGCGCATATTTATGTGTGTG 1947

Db 1667 GAGACAGGAAACACCTGTGAAGCTGATCCAGAGCGCGTCCCATCTATGTGTGCG 1726
QY 1948 GAGATGCAAGAAATTTGGCCCAAGTGTACA 1978
DB 1727 GGGATGCTCGAAATATGGCCAAAGATGTGCA 1757

RESULT 9

US-09-917-800A-1397
; Sequence 1397, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1397
; LENGTH: 2401
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 M10068
US-09-917-800A-1397

Query Match 4.0%; Score 83; DB 11; Length 2401;
Best Local Similarity 55.2%; Pred. No. 3.2e-15;
Matches 216; Conservative 0; Mismatches 155; Indels 20; Gaps 2;

QY 1588 TTCACCTTACAGATGATGACCCCTCATTCCTCATATATGTTGGTCCAGAACCGGCATA 1647
DB 1556 TTCCTCTTCCCTTTCAGTCCACACACCTGTCATATGTTGGCCCGGCATGGGATT 1615
QY 1648 GCGCCGTTTATTTGGTCTCTACATCAATGAATCAAGAACACACCCAGATGGAATT 1707
DB 1616 GCGCTTTCATGCGCTTATCATCAGAGAGAGCTTGCTT--CGAAGCAAGCAAGAGAG 1673
QY 1708 TTGAGCAATGTGTTGTTTGGCTGACAGCATTAAGATAGGATTATCTATTCAGAA 1767
DB 1674 TGGGAGAGACGCTGCTATACATATGCTGCGCGCTCGATGAGACTATCTGACCGTG 1733
QY 1768 AAGACTCAGACATTTCTTAAGCATGGATTTAATCATTAAGTTTCTCTCTCAA 1827
DB 1734 AAGACTGAGCCGCTTCCACAGAGAGCGTCCCTCAGCAGCTTATGTTGGCTTTTCCC 1793
QY 1828 GAGATGCTCTGTTGGGAGAGAGAGCCCGCAGCAAGATATGATACAGACATCCAGC 1887
DB 1794 G-----GGAGCAGGCCCAAGGTCTATGTCCAGCACCTTCTGAAAGA 1835

Db 62 TTAGAGGCTTCTTGACAGAAAGTTACATTGA--AACAACTGGGGCAGAAATTGGGCA 119
QY 1714 CAAGTGGTGTGTTTGGTGCAGGCAATAGAGATTATATTCAGAAAGGC 1773
Db 120 CTTCAATCTTTCTTGGATGACAGAACCGTAATATGACTACATAATGAAAGTAGT 179
QY 1774 TCAGACATTTCTTAAGCATGGATCTTAAGTCAATCAAGGTTCTTCT 1824
Db 180 TGCAAACTTCTTGANAGAGGGGGCTTCTGAGCTAATGTTGCAATCT 230

RESULT 13
US-09-822-849A-278
; Sequence 278, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6A03
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 278
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-278

Query Match 2.9%; Score 60.4; DB 10; Length 2470;
Best Local Similarity 53.7%; Pred. No. 6.5e-08;
Matches 136; Conservative 0; Mismatches 106; Indels 2; Gaps 1;

QY 1588 TTCCACTACAGATGACCCCTCAATCCCATATATGATGGGGCCAGGAACGGGCATA 1647
Db 1615 TTCCGCGCTGCGCTTCAAGGCCACACGCGCTGTATCATATGATGGGGCCGCGCGGGTG 1674
QY 1648 GCGCCGTTTATTTGGTCTTCAACATAGAAACTCCAGAACACACCCAGATGGAATT 1707
Db 1675 GCACCCCTCATAGGCTTATCATCAGAGGCGGGCTGGTG--CGACAGCAGGGCAGAGAG 1732
QY 1708 TTGGAGCAATGTGTTGTTTGGTCTGAGCATAGAGATATCTATTTCAGAA 1767
Db 1733 TGGGGAGACGCTGCTGACTACAGGCTGCCCGCTCGAGTAGAGACTACATCTGCCGG 1792
QY 1768 AAGACCTCAGACATTTCTTAAGCATGGATCTTAAGTCAATCAAGGTTCTTCTCAA 1827
Db 1793 AGGAGCTGGCGAGTTCACAGAGGAGCGGTGGCTCACCAGCTCAAGGCTTCTCTCC 1852
QY 1828 GAGA 1831
Db 1853 GGGA 1856

RESULT 14
US-09-938-842A-803
; Sequence 803, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kieps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 803
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-803

Query Match 2.8%; Score 58.4; DB 11; Length 2136;
Best Local Similarity 54.8%; Pred. No. 2.6e-07;
Matches 137; Conservative 0; Mismatches 111; Indels 2; Gaps 1;

QY 1588 TTCCACTACAGATGACCCCTCAATCCCATATATGATGGGTCCAGAACCGGCATA 1647
Db 1657 TTCAAGCTTCTTGTATTTCAAGGTACCATCATCATGATCGGTCCAGGAGTGATTA 1716
QY 1648 GCGCCGTTTATTTGGTCTTCAACATAGAACTCCAGAACACACCCAGATGGAATT 1707
Db 1717 GCTCATTCAGAGAGTTCCTTCAGAGAAAGATAGCGTTGGT--AGAACTGCTGTGTAAC 1774
QY 1708 TTGGAGCAATGTGTTTGGTCTGAGCATAGAGATATGATTTATTCAGAA 1767
Db 1775 TTGGGCCATCACTTTGTTTCTTTGGATCAGAAACCGTAGATTTCTATTCAGAG 1834
QY 1768 AAGACCTCAGACATTTCTTAAGCATGGATCTTAAGTCAATCAAGGTTCTTCTCAA 1827
Db 1835 AAGACCTCAGAGATTTGTTGAGAGTGTGCTGCGAGAGTAAAGTGTGCGCTTCTCTC 1894
QY 1828 GAGATCTCC 1837
Db 1895 GTGAAGGAC 1904

RESULT 15
US-09-765-873A-13
; Sequence 13, Application US/09765873A
; Patent No. US20010053847A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009 US CIP
; CURRENT APPLICATION NUMBER: US/09/765,873A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/627,216
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Helianthus tuberosus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1764)
US-09-765-873A-13

Query Match 2.7%; Score 56; DB 10; Length 1863;
Best Local Similarity 49.0%; Pred. No. 1.4e-06;
Matches 253; Conservative 0; Mismatches 240; Indels 23; Gaps 3;

QY 1576 ACAACAATTTCTTTCACCTTACAGATGACCCCTCAATCCCATCATATGATGGTGCA 1635

